

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2005, 21:43:38 ; Search time 43 Seconds
(without alignments)
387.134 Million cell updates/sec

Title: US-10-723-123-3
Perfect score: 1194
Sequence: 1 MPLNLGDSFPDFOAALGAE.....EALQLPSGKPYLRLTPDPRG 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1194	100.0	223	3	US-09-411-578-3
2	1194	100.0	223	4	US-09-749-233-3
3	640.5	53.6	235	3	US-08-862-540-9
4	640.5	53.6	235	3	US-09-633-043-9
5	637.5	53.4	223	4	US-09-538-092-1038
6	618.5	51.8	235	3	US-08-862-540-2
7	618.5	51.8	235	3	US-09-633-043-2
8	498.5	41.8	224	4	US-09-270-767-43949
9	497.5	41.7	222	4	US-09-252-991A-16816
10	494.5	41.4	216	4	US-09-328-352-5328
11	453	37.9	257	4	US-09-248-796A-20366
12	413.5	34.6	161	4	US-09-202-329-15
13	256.5	21.5	116	4	US-09-270-767-43977
14	222	18.6	184	4	US-09-902-540-10665
15	205	17.2	194	4	US-09-202-329-10
16	199	16.7	982	4	US-09-551-974A-95
17	199	16.7	982	4	US-09-565-501A-95
18	199	16.7	982	4	US-09-639-206A-95
19	199	16.7	982	4	US-09-874-923-95
20	199	16.7	1427	4	US-09-551-974A-97
21	199	16.7	1427	4	US-09-565-501A-97
22	199	16.7	1427	4	US-09-639-206A-97
23	199	16.7	1427	4	US-09-874-923-97
24	199	16.7	1641	4	US-09-551-974A-96
25	199	16.7	1641	4	US-09-565-501A-96
26	199	16.7	1641	4	US-09-639-206A-96
27	199	16.7	1641	4	US-09-874-923-96

28	196.5	16.5	195	4	US-09-556-877-65	Sequence 65, Appl
29	196.5	16.5	195	4	US-09-620-412C-65	Sequence 65, Appl
30	196.5	16.5	195	4	US-09-410-568-65	Sequence 65, Appl
31	196.5	16.5	195	4	US-09-588-419-65	Sequence 65, Appl
32	196.5	16.5	196	4	US-09-556-877-294	Sequence 294, App
33	196.5	16.5	196	4	US-09-620-412C-294	Sequence 294, App
34	196.5	16.5	196	4	US-09-598-419-294	Sequence 294, App
35	196.5	16.5	202	4	US-09-556-877-92	Sequence 92, Appl
36	196.5	16.5	202	4	US-09-620-412C-92	Sequence 92, Appl
37	196.5	16.5	202	4	US-09-410-568-92	Sequence 92, Appl
38	196.5	16.5	202	4	US-09-598-419-92	Sequence 92, Appl
39	193.5	16.2	195	4	US-08-311-731A-84	Sequence 84, Appl
40	193	16.2	231	4	US-09-438-185A-780	Sequence 780, App
41	192.5	16.1	198	4	US-09-202-329-13	Sequence 13, Appl
42	191	16.0	199	2	US-08-467-265-17	Sequence 17, Appl
43	191	16.0	199	3	US-08-467-265-17	Sequence 17, Appl
44	191	16.0	199	3	US-09-407-891-17	Sequence 17, Appl
45	189	15.8	204	4	US-09-252-991A-17611	Sequence 17611, A

ALIGNMENTS

RESULT 1
US-09-411-578-3
; Sequence 3, Application US/09411578
; Patent No. 6203801
; GENERAL INFORMATION:
; APPLICANT: Schaap, Theodorus C
; APPLICANT: Kuiper, Catharina M
; TITLE OF INVENTION: Coccidiosis Vaccines
; FILE REFERENCES: schaa
; CURRENT APPLICATION NUMBER: US/09/411,578
; CURRENT FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 98203384.7
; EARLIER FILING DATE: 1998-10-07
; EARLIER APPLICATION NUMBER: 98203457.1
; EARLIER FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Eimeria tenella
US-09-411-578-3

Query Match	100.0%;	Score 1194;	DB 3;	Length 223;
Best Local Similarity	100.0%;	Pred. No. 6.2e-133;		
Matches 223;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	MPLNLGDSFPDFOAALGAEHRLHLYLGD	SWGWMF	SHPNDFTPVCTT
Db	1	MPLNLGDSFPDFOAALGAEHRLHLYLGD	SWGWMF	SHPNDFTPVCTT
Qy	61	TKNKCKLVGFSCNDLQSHREWAKDINAYAGRS	GNLFPPLVCDN	RELAASLGIMDPAEKD
Db	61	TKNKCKLVGFSCNDLQSHREWAKDINAYAGRS	GNLFPPLVCDN	RELAASLGIMDPAEKD
Qy	121	KKGLPLTCRCVFFISPEKKLAASILYPATTGR	NFABILRVLD	SLQLTAKFPVATPDWTA
Db	121	KKGLPLTCRCVFFISPEKKLAASILYPATTGR	NFABILRVLD	SLQLTAKFPVATPDWTA
Qy	181	GAKCCVPMIAEAEARLLPKGHEALQLPSGKPYL	RLTPDPRG	223
Db	181	GAKCCVPMIAEAEARLLPKGHEALQLPSGKPYL	RLTPDPRG	223

RESULT 2
US-09-749-233-3
; Sequence 3, Application US/09749233
; Patent No. 6680061
; GENERAL INFORMATION:

```
; APPLICANT: Schaap, Theodorus C
; APPLICANT: Kuiper, Catharina M
; APPLICANT: Vermeulen, Arnoldus N
; TITLE OF INVENTION: Coccidiosis Vaccines
; FILE REFERENCE: schaap
; CURRENT APPLICATION NUMBER: US/09/749,233
; CURRENT FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 09/411,578
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 98203457.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Eimeria tenella
US-09-749-233-3

Query Match 100.0%; Score 1194; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 6.2e-133;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPLNLGDSPPDFOAEALGAEHFRLHEYLGDWGVMSFHPNDFTPVCTTTELAAVAKLQDSF 60
DB 1 MPLNLGDSPPDFOAEALGAEHFRLHEYLGDWGVMSFHPNDFTPVCTTTELAAVAKLQDSF 60

QY 61 TKKNCKLVGSCNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGMTDPAEKD 120
DB 61 TKKNCKLVGSCNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGMTDPAEKD 120

QY 121 KKGPLTCRCVFFISPEKKLAASILYPATTGRNFASILRVLDLSQLTAKFPVATPDWTA 180
DB 121 KKGPLTCRCVFFISPEKKLAASILYPATTGRNFASILRVLDLSQLTAKFPVATPDWTA 180

QY 181 GAKCCVVPNLAAEAOQLPKGHEALQPSGKPYLRLTPDPRG 223
DB 181 GAKCCVVPNLAAEAOQLPKGHEALQPSGKPYLRLTPDPRG 223

RESULT 3
US-08-862-540-9
; Sequence 9, Application US/08862540
; Patent No. 6150135
; GENERAL INFORMATION:
; APPLICANT: Ramaswamy Chandrashekar
; APPLICANT: Naotoshi Tsuji
; TITLE OF INVENTION: DIROFILARIA AND BRUGIA THIOREDOXIN
; TITLE OF INVENTION: PEROXIDASE TYPE-2 (TPX-2) PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,540
; FILING DATE: MAY 23, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: HW-4
```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-862-540-9

Query Match 53.6%; Score 640.5; DB 3; Length 235;
Best Local Similarity 55.5%; Pred. No. 2.5e-67;
Matches 127; Conservative 29; Mismatches 62; Indels 11; Gaps 3;

QY 5 LGDSPPDFOAEALGAEHFRLHEYLGDWGVMSFHPNDFTPVCTTTELAAVAKLQDSFTKK 63
DB 7 LGDKFPDFOAETSESFISSFHDMIGKDSWAILFSDHPRDFTPVCTTTELARLVQLEPEPKR 66

QY 64 NCKLVGSCNDLQSHREWAKDIMAYAGR-----SGN-LPFPVCDPNRELAASLGI 113
DB 67 NVKLGSLCSDVQSHRKWADDIIELCRMKSGDSNTCCSGNKLFPPIADNRSLSKLG 126

QY 114 MPAEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVA 173
DB 127 MPDDECEDEGAALTARCLFIIGPEKTLKUSILYPATTGRNFBELRVLDLSQLTATKLVA 186

QY 174 TPVDWTAGACCCVVPNLAAEAOQLPKGHEALQPSGKPYLRLTPDPR 222
DB 187 TPVDWQNGDCVVVPTINDNEAKLFGKINTVELPSGKRYLRMVAHPK 235

RESULT 4
US-09-633-043-9
; Sequence 9, Application US/09633043
; Patent No. 6352836
; GENERAL INFORMATION:
; APPLICANT: Ramaswamy Chandrashekar
; APPLICANT: Naotoshi Tsuji
; TITLE OF INVENTION: DIROFILARIA AND BRUGIA THIOREDOXIN
; TITLE OF INVENTION: PEROXIDASE TYPE-2 (TPX-2) PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/633,043
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/862,540
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: HW-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-633-043-9

Query Match      53.6%; Score 640.5; DB 3; Length 235;
Best Local Similarity 55.5%; Pred. No. 2.5e-67;
Matches 127; Conservative 29; Mismatches 62; Indels 11; Gaps 3;

QY 5 LGDSFPDFOAEALGAEHFRLHEYLGD-SWGMVFSHPNDFTPVCTTLEAAVKLQDSFTKK 63
Db 7 LGDFFPDFOAEALGAEHFRLHEYLGD-SWGMVFSHPNDFTPVCTTLEAAVKLQDSFTKK 66
QY 64 NCKLVGFCNDLQSHREWAKDIMAYAGR-----SGN-LPPPLVCDPNRELAASLGI 113
Db 67 NVKLIGLSCDSVQSHRWADDIIELCRMKSGDSNCCSGNKLPPFIADNRSLSKLG 126
QY 114 MDAEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVA 173
Db 127 MDPDECDKGAALTARCLFIIGPEKTLKLSILYPATTGRNFAEILRVLDLSQLTAKLVA 186
QY 174 TPVDWTAGKCCVVPNLAAEAQRLLPKGHEALQIPSGKPYRLTPDPR 222
Db 187 TPVDWQNGDDCVVVFPTINDNEAKKLFGEKINTVLPSPGKPYRLTPDPR 235

RESULT 5
US-09-538-092-1038
; Sequence 1038, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqformatter Version 0.9
; SEQ ID NO 1038
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P30041
US-09-538-092-1038

Query Match      53.4%; Score 637.5; DB 4; Length 223;
Best Local Similarity 56.6%; Pred. No. 5.3e-67;
Matches 125; Conservative 28; Mismatches 65; Indels 3; Gaps 2;

QY 3 LNLGDSFPDFOAEALGAEHFRLHEYLGD-SWGMVFSHPNDFTPVCTTLEAAVKLQDSFTK 62
Db 4 LLLGDVAPNFEANTT-VGRIRFHDHFLGDSWGLFSDHPRDFTPVCTTLEAAVKLQDSFTK 62
QY 63 KCKLVGFCNDLQSHREWAKDIMAYAGR-----SGN-LPPPLVCDPNRELAASLGI 120
Db 63 RNVKLIALSDSDVDEHLAWSKDINAYNCEBTEKLPFIIDDRNRELAALLGMLDPAEKD 122
QY 121 KKGGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPDWTA 180
Db 123 EKGMPVTARVVVFGPDKLLKLSILYPATTGRNFAEILRVLDLSQLTAKFPVATPDWTD 182
QY 181 GAKCCVVPNLAAEAQRLLPKGHEALQIPSGKPYRLTPDPR 221
Db 183 GDSVMVLPFTTPEEAKKLPFGVFTKELPSGKPYRLTPDPR 223
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RESULT 6
US-08-862-540-2
; Sequence 2, Application US/08862540
; Patent No. 6150135
; GENERAL INFORMATION:
; APPLICANT: Ramaswamy Chandrashekar
; APPLICANT: Naotoshi Teuji
; TITLE OF INVENTION: DIROFILARIA AND BRUGIA THIOREDOXIN
; TITLE OF INVENTION: PEROXIDASE TYPE-2 (TPX-2) PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA: US/08/862,540
; APPLICATION NUMBER: US/08/862,540
; FILING DATE: MAY 23, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: HW-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-862-540-2

Query Match      51.8%; Score 618.5; DB 3; Length 235;
Best Local Similarity 54.1%; Pred. No. 1e-64;
Matches 124; Conservative 28; Mismatches 66; Indels 11; Gaps 3;

QY 5 LGDSFPDFOAEALGAEHFRLHEYLGD-SWGMVFSHPNDFTPVCTTLEAAVKLQDSFTKK 63
Db 7 LGDKFPDFAETNEGFIPIPSYDWIGKSWAILFSHPRDFTPVCTTLEARLVQLAPEPKR 66
QY 64 NCKLVGFCNDLQSHREWAKDIMAYAGR-----SGN-LPPPLVCDPNRELAASLGI 113
Db 67 NVKLIGLSCDSAESHRKWDIDINAVCKMKCNDGDTCCSGNKLPPFIADNRSFLATELGM 126
QY 114 MDAEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVA 173
Db 127 MDPDERDENGNALTARCVFTIIGPEKTLKLSILYPATTGRNFAEILRVLDLSQLTAKLVA 186
QY 174 TPVDWTAGKCCVVPNLAAEAQRLLPKGHEALQIPSGKPYRLTPDPR 222
Db 187 TPVDWQNGDDCVVVFPTINDTEAKKLFGEKINTVLPSPGKPYRLTPDPR 235

RESULT 7
US-09-633-043-2
; Sequence 2, Application US/09633043
; Patent No. 6352836
; GENERAL INFORMATION:
; APPLICANT: Ramaswamy Chandrashekar
```



```

; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Peter Probst
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C6
; CURRENT APPLICATION NUMBER: US/09/565.501A
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 982
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-565-501A-95

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Query Match      16.7%; Score 199; DB 4; Length 982;
Best Local Similarity 27.4%; Pred. No. 4.7e-14;
Matches 58; Conservative 35; Mismatches 91; Indels 28; Gaps 8;

QY 10 PDFQAEAL-----GAEHFRLHLYLGDSDGVMFSPHNDFTPVCTTTELAAVAKLQDS---FTK 62
DB 20 PSFEVALMPNGSPFKISLSSYKG-KWVLFYFLDFTFVCPTFV---IAFSDSVSRFNE 75
QY 63 KNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPAEKDKK 122
DB 76 LNCVELACSIDSEYAHLOWTLQDRKKG-LGTWAIPLMLADTKTSIARSYGVLEESQ---- 130
QY 123 GLPLTCRCVFFISPEKKLAASILYPATTGRNFABILRVLSLQLTAKFPVATPVDMWTAGA 182
DB 131 --GVAYRGLFIIDPHGMLRQITVNDMPVGRSVBEVLRLLEAFQFVEKHGEVCPANWKGA 188
QY 183 KCC--VWNLAAE-----EAQRLLPKGHE 204
DB 189 PTMKPEPNASVEGYFSKQSGMDATLKNKGNE 220

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RESULT 18
US-09-639-206A-95
; Sequence 95, Application US/09639206A
; Patent No. 661337
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C7
; CURRENT APPLICATION NUMBER: US/09/639.206A
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 982
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-639-206A-95

```

```

Query Match      16.7%; Score 199; DB 4; Length 982;
Best Local Similarity 27.4%; Pred. No. 4.7e-14;
Matches 58; Conservative 35; Mismatches 91; Indels 28; Gaps 8;

QY 10 PDFQAEAL-----GAEHFRLHLYLGDSDGVMFSPHNDFTPVCTTTELAAVAKLQDS---FTK 62
DB 20 PSFEVALMPNGSPFKISLSSYKG-KWVLFYFLDFTFVCPTFV---IAFSDSVSRFNE 75
QY 63 KNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPAEKDKK 122
DB 76 LNCVELACSIDSEYAHLOWTLQDRKKG-LGTWAIPLMLADTKTSIARSYGVLEESQ---- 130
QY 123 GLPLTCRCVFFISPEKKLAASILYPATTGRNFABILRVLSLQLTAKFPVATPVDMWTAGA 182
DB 131 --GVAYRGLFIIDPHGMLRQITVNDMPVGRSVBEVLRLLEAFQFVEKHGEVCPANWKGA 188
QY 183 KCC--VWNLAAE-----EAQRLLPKGHE 204
DB 189 PTMKPEPNASVEGYFSKQSGMDATLKNKGNE 220

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RESULT 19
US-09-874-923-95
; Sequence 95, Application US/09874923
; Patent No. 6638517
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; APPLICANT: Brannon, Mark
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C8
; CURRENT APPLICATION NUMBER: US/09/874.923
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 982
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-874-923-95

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```

Query Match      16.7%; Score 199; DB 4; Length 982;
Best Local Similarity 27.4%; Pred. No. 4.7e-14;
Matches 58; Conservative 35; Mismatches 91; Indels 28; Gaps 8;

QY 10 PDFQAEAL-----GAEHFRLHLYLGDSDGVMFSPHNDFTPVCTTTELAAVAKLQDS---FTK 62
DB 20 PSFEVALMPNGSPFKISLSSYKG-KWVLFYFLDFTFVCPTFV---IAFSDSVSRFNE 75
QY 63 KNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPAEKDKK 122
DB 76 LNCVELACSIDSEYAHLOWTLQDRKKG-LGTWAIPLMLADTKTSIARSYGVLEESQ---- 130
QY 123 GLPLTCRCVFFISPEKKLAASILYPATTGRNFABILRVLSLQLTAKFPVATPVDMWTAGA 182
DB 131 --GVAYRGLFIIDPHGMLRQITVNDMPVGRSVBEVLRLLEAFQFVEKHGEVCPANWKGA 188
QY 183 KCC--VWNLAAE-----EAQRLLPKGHE 204
DB 189 PTMKPEPNASVEGYFSKQSGMDATLKNKGNE 220

```

```
RESULT 20
US-09-551-974A-97
; Sequence 97, Application US/09551974A
; Patent No. 6500437
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillion, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121.420C5
; CURRENT APPLICATION NUMBER: US/09/551,974A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 1427
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-551-974A-97

Query Match      16.7%; Score 199; DB 4; Length 1427;
Best Local Similarity 27.4%; Pred. No. 8.4e-14;
Matches 58; Conservative 35; Mismatches 91; Indels 28; Gaps 8;

QY 10 PDFQAEAL-----GAEHFRLHEYLGDGSGWMFSPNDFTPVCTTELAEAVKLQDS---FTK 62
DB 20 PSFEEVALMPNGSFKKISLSYKG-KWVVLFFYPDLDTFVCPTFV---IAFSDSVSRFNE 75
QY 63 KNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPASKDKK 122
DB 76 LNCEVLACSIDSEYAHLOWTLQDRKKG-LGTWAIPLADTKTSIARSYGVLESQ---- 130
QY 123 GLPLTCRCVFFISPEKKLAASILYPATTGRNFAELRLVLDLSQLTAKFPVATPDVDTAG 182
DB 131 --GVAYRGLFIIDPHGMLRQITVNDMPVGRSVVEVLRLLEAFQFVEKHGVCVPANWKGA 188
QY 183 KCC-VVPNLAAE-----EAQRLLPKGHE 204
DB 189 PTMKPEPNASVEGYFSKQSGMDATLKNKGNE 220

RESULT 21
US-09-565-501A-97
; Sequence 97, Application US/09565501A
; Patent No. 6607731
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillion, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Peter Probst
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121.420C6
; CURRENT APPLICATION NUMBER: US/09/565,501A
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 1427
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple

US-09-565-501A-97
; Sequence 97, Application US/09639206A
; Patent No. 6613337
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillion, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121.420C7
; CURRENT APPLICATION NUMBER: US/09/639,206A
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 1427
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-639-206A-97

Query Match      16.7%; Score 199; DB 4; Length 1427;
Best Local Similarity 27.4%; Pred. No. 8.4e-14;
Matches 58; Conservative 35; Mismatches 91; Indels 28; Gaps 8;

QY 10 PDFQAEAL-----GAEHFRLHEYLGDGSGWMFSPNDFTPVCTTELAEAVKLQDS---FTK 62
DB 20 PSFEEVALMPNGSFKKISLSYKG-KWVVLFFYPDLDTFVCPTFV---IAFSDSVSRFNE 75
QY 63 KNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPASKDKK 122
DB 76 LNCEVLACSIDSEYAHLOWTLQDRKKG-LGTWAIPLADTKTSIARSYGVLESQ---- 130
QY 123 GLPLTCRCVFFISPEKKLAASILYPATTGRNFAELRLVLDLSQLTAKFPVATPDVDTAG 182
DB 131 --GVAYRGLFIIDPHGMLRQITVNDMPVGRSVVEVLRLLEAFQFVEKHGVCVPANWKGA 188
QY 183 KCC-VVPNLAAE-----EAQRLLPKGHE 204
DB 189 PTMKPEPNASVEGYFSKQSGMDATLKNKGNE 220
```

```
; OTHER INFORMATION: Leishmania antigens
US-09-565-501A-97

Query Match      16.7%; Score 199; DB 4; Length 1427;
Best Local Similarity 27.4%; Pred. No. 8.4e-14;
Matches 58; Conservative 35; Mismatches 91; Indels 28; Gaps 8;

QY 10 PDFQAEAL-----GAEHFRLHEYLGDGSGWMFSPNDFTPVCTTELAEAVKLQDS---FTK 62
DB 20 PSFEEVALMPNGSFKKISLSYKG-KWVVLFFYPDLDTFVCPTFV---IAFSDSVSRFNE 75
QY 63 KNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPASKDKK 122
DB 76 LNCEVLACSIDSEYAHLOWTLQDRKKG-LGTWAIPLADTKTSIARSYGVLESQ---- 130
QY 123 GLPLTCRCVFFISPEKKLAASILYPATTGRNFAELRLVLDLSQLTAKFPVATPDVDTAG 182
DB 131 --GVAYRGLFIIDPHGMLRQITVNDMPVGRSVVEVLRLLEAFQFVEKHGVCVPANWKGA 188
QY 183 KCC-VVPNLAAE-----EAQRLLPKGHE 204
DB 189 PTMKPEPNASVEGYFSKQSGMDATLKNKGNE 220

RESULT 22
US-09-639-206A-97
; Sequence 97, Application US/09639206A
; Patent No. 6613337
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillion, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121.420C7
; CURRENT APPLICATION NUMBER: US/09/639,206A
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 1427
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-639-206A-97

Query Match      16.7%; Score 199; DB 4; Length 1427;
Best Local Similarity 27.4%; Pred. No. 8.4e-14;
Matches 58; Conservative 35; Mismatches 91; Indels 28; Gaps 8;

QY 10 PDFQAEAL-----GAEHFRLHEYLGDGSGWMFSPNDFTPVCTTELAEAVKLQDS---FTK 62
DB 20 PSFEEVALMPNGSFKKISLSYKG-KWVVLFFYPDLDTFVCPTFV---IAFSDSVSRFNE 75
QY 63 KNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPASKDKK 122
DB 76 LNCEVLACSIDSEYAHLOWTLQDRKKG-LGTWAIPLADTKTSIARSYGVLESQ---- 130
QY 123 GLPLTCRCVFFISPEKKLAASILYPATTGRNFAELRLVLDLSQLTAKFPVATPDVDTAG 182
DB 131 --GVAYRGLFIIDPHGMLRQITVNDMPVGRSVVEVLRLLEAFQFVEKHGVCVPANWKGA 188
QY 183 KCC-VVPNLAAE-----EAQRLLPKGHE 204
DB 189 PTMKPEPNASVEGYFSKQSGMDATLKNKGNE 220
```

```
RESULT 23
US-09-874-923-97
; Sequence 97, Application US/09874923
; Patent No. 6638517
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; APPLICANT: Brannon, Mark
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C8
; CURRENT APPLICATION NUMBER: US/09/874, 923
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 1427
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-874-923-97

Query Match 16.7%; Score 199; DB 4; Length 1427;
Best Local Similarity 27.4%; Pred. No. 8.4e-14;
Matches 58; Conservative 35; Mismatches 91; Indels 28; Gaps 8;

QY 10 PDFQAEAL----GAEHFRLHEYLGDSDGWMFSPNDFTPVCTTTELAEAVKLQDS----FTK 62
Db 20 PSFEVALMPNGSFKKISLSYKG-KWVLFYPLDFTVCPTTEV---IAFSDSVSRFNE 75
QY 63 KNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPFLVCDPNRELAASLGIMDPAEKDKK 122
Db 76 LNCVELACSIDSEYAHQWTLQDRKKG-LGTWAIPLADTKTSIARSYGVLESQ---- 130
QY 123 GLPLTCRCVFFISPEKKLAASILYPATGRNFAEILRVLDLSLQLTAKFPVATPVDWTAGA 182
Db 131 --GVAYRGLFIIDPHGMLRQITVNDMPVGRSVEEVLRLLEAFQFVEKHGEVCPANWKKA 188
QY 183 KCC-VVFNLAEE-----EAQRLLPKGHE 204
Db 189 PTMKPEPNASVEGYFSKQSGMDATLKNKGNE 220

RESULT 24
US-09-551-974A-96
; Sequence 96, Application US/09551974A
; Patent No. 6500437
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C5
; CURRENT APPLICATION NUMBER: US/09/551, 974A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 1641
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-551-974A-96

Query Match 16.7%; Score 199; DB 4; Length 1641;
Best Local Similarity 27.4%; Pred. No. 1e-13;
Matches 58; Conservative 35; Mismatches 91; Indels 28; Gaps 8;

QY 10 PDFQAEAL----GAEHFRLHEYLGDSDGWMFSPNDFTPVCTTTELAEAVKLQDS----FTK 62
Db 20 PSFEVALMPNGSFKKISLSYKG-KWVLFYPLDFTVCPTTEV---IAFSDSVSRFNE 75
QY 63 KNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPFLVCDPNRELAASLGIMDPAEKDKK 122
Db 76 LNCVELACSIDSEYAHQWTLQDRKKG-LGTWAIPLADTKTSIARSYGVLESQ---- 130
QY 123 GLPLTCRCVFFISPEKKLAASILYPATGRNFAEILRVLDLSLQLTAKFPVATPVDWTAGA 182
Db 131 --GVAYRGLFIIDPHGMLRQITVNDMPVGRSVEEVLRLLEAFQFVEKHGEVCPANWKKA 188
QY 183 KCC-VVFNLAEE-----EAQRLLPKGHE 204
Db 189 PTMKPEPNASVEGYFSKQSGMDATLKNKGNE 220

RESULT 25
US-09-565-501A-96
; Sequence 96, Application US/09565501A
; Patent No. 6607731
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Peter Probst
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C6
; CURRENT APPLICATION NUMBER: US/09/565, 501A
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 1641
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-565-501A-96

Query Match 16.7%; Score 199; DB 4; Length 1641;
Best Local Similarity 27.4%; Pred. No. 1e-13;
Matches 58; Conservative 35; Mismatches 91; Indels 28; Gaps 8;

QY 10 PDFQAEAL----GAEHFRLHEYLGDSDGWMFSPNDFTPVCTTTELAEAVKLQDS----FTK 62
Db 20 PSFEVALMPNGSFKKISLSYKG-KWVLFYPLDFTVCPTTEV---IAFSDSVSRFNE 75
QY 63 KNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPFLVCDPNRELAASLGIMDPAEKDKK 122
Db 76 LNCVELACSIDSEYAHQWTLQDRKKG-LGTWAIPLADTKTSIARSYGVLESQ---- 130
QY 123 GLPLTCRCVFFISPEKKLAASILYPATGRNFAEILRVLDLSLQLTAKFPVATPVDWTAGA 182
Db 131 --GVAYRGLFIIDPHGMLRQITVNDMPVGRSVEEVLRLLEAFQFVEKHGEVCPANWKKA 188
QY 183 KCC-VVFNLAEE-----EAQRLLPKGHE 204
Db 189 PTMKPEPNASVEGYFSKQSGMDATLKNKGNE 220
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Db 189 PTWKPEPNASVEGYFSKQSGMDATELKNKGNE 220

RESULT 26
US-09-639-206A-96
; Sequence 96, Application US/09639206A
; Patent No. 6613337
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121.420C7
; CURRENT APPLICATION NUMBER: US/09/639,206A
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 1641
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-639-206A-96

Query Match 16.7%; Score 199; DB 4; Length 1641;
Best Local Similarity 27.4%; Pred. No. 1e-13;
Matches 58; Conservative 35; Mismatches 91; Indels 28; Gaps 8;

Qy 10 PDFQAEAL----GAEHFRLHLYGDSWGMFSGHPNDFTPVCTTELAEEAVKLQDS---FTK 62
Db 20 PSFEVALMPNGSFKKISLSYKG-KWVLFYFPLDFTFVCPTEV---IAPSDSVSRNE 75
Qy 63 KNCKLVGSCNDLQSHREWAKOIMAYAGRSNLPPLVCDPNRELAASLGIMDPAEKDKK 122
Db 76 LNCEVLACSDSEYAHQLWTLQDRKKG-LGTMAIPMLADTKTSIARSYGVLEESQ---- 130
Qy 123 GLPLTCRCVFFISPEKKLAASILYPATTCGRNFAELRLVLDLSQLTAKFPVATPDWTAGA 182
Db 131 --GVAYRGLFIIDPHGMLRQITVNDMPVGRSVEEVLRLLEAFQFVEKHGEVCPANWKKA 188
Qy 183 KCC-VVNPAAE-----EAQRLLPKGHE 204
Db 189 PTWKPEPNASVEGYFSKQSGMDATELKNKGNE 220

RESULT 27
US-09-556-877-65
; Sequence 65, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 65
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-556-877-65

Query Match 16.5%; Score 196.5; DB 4; Length 195;
Best Local Similarity 29.6%; Pred. No. 7.5e-15;
Matches 55; Conservative 37; Mismatches 75; Indels 19; Gaps 8;

Qy 5 LGDSFPDQAEAL--GAE-HFRLHLYGDSWGMFSGHPNDFTPVCTTEL-AEAVKLQDSF 60
Db 5 VGRQAPDFSGKAVVCGEKEISLADPRG-KYVVLFFYPKDFTYVCTTELHAFQDRLDV-F 62
Qy 61 TKCNCKLVGSCNDLQSHREW---AKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPA 117
Db 63 EEHGAVVLGCVSDDIETHSRWLTAVND----AGGIEGTETPLADPSFKISAEFGVLNPE 118
Qy 118 EKDKGLPLTCRCVFFISPEKKLAASILYPATTCGRNFAELRLVLDLSQLTAKFPVATPD 177
Db 119 GS-----LALRATFLDKHGVRHNAVINDLPLGRSIDEELRLDLSLFFENHGVCPAN 172
Qy 178 WTAGAK 183
Db 173 WRSRG 178

```

```
RESULT 29
US-09-620-412C-65
; Sequence 65, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620.412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 65
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-65

Query Match 16.5%; Score 196.5; DB 4; Length 195;
Best Local Similarity 29.6%; Pred. No. 7.5e-15;
Matches 55; Conservative 37; Mismatches 75; Indels 19; Gaps 8;

Qy 5 LGDSFPDQAEAL--GAE-HFRLHEYLGDGVMFHPNDFTPVCTTEL-AEAVKLQDSF 60
: ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 5 VGRQAPDFSGKAVVCGEKEISLADFRG-KYVVLFFYPKDFTYVCPTELHAFQDRLDV-F 62

Qy 61 TKNCKLVGSCNDLQSHREW---AKDIMAYAGSGNLPPLVCDPNRELAASLGIMDPA 117
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 EHGAVVLGCVDDIETHSRWLTWARD---AGGIEGTEYPLLADPSFKISEAFGLNPE 118

Qy 118 EKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPVD 177
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 GS-----LALRATFLIDKHGVIHAVINDPLGRSIDELRLDLSLIPFENHGMVCPAN 172

Qy 178 WTAGAK 183
: : :
Db 173 WRSGER 178

RESULT 30
US-09-410-568-65
; Sequence 65, Application US/09410568
; Patent No. 6555115
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fang, Hang
; APPLICANT: Jen, Shyian
; APPLICANT: Stromberg, Erica Jean
; APPLICANT: Enghart, Susan E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C2
; CURRENT APPLICATION NUMBER: US/09/410.568
; CURRENT FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 65
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-410-568-65

Query Match 16.5%; Score 196.5; DB 4; Length 195;
Best Local Similarity 29.6%; Pred. No. 7.5e-15;
Matches 55; Conservative 37; Mismatches 75; Indels 19; Gaps 8;

Qy 5 LGDSFPDQAEAL--GAE-HFRLHEYLGDGVMFHPNDFTPVCTTEL-AEAVKLQDSF 60
: ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 5 VGRQAPDFSGKAVVCGEKEISLADFRG-KYVVLFFYPKDFTYVCPTELHAFQDRLDV-F 62

Qy 61 TKNCKLVGSCNDLQSHREW---AKDIMAYAGSGNLPPLVCDPNRELAASLGIMDPA 117
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 EHGAVVLGCVDDIETHSRWLTWARD---AGGIEGTEYPLLADPSFKISEAFGLNPE 118

Qy 118 EKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPVD 177
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 GS-----LALRATFLIDKHGVIHAVINDPLGRSIDELRLDLSLIPFENHGMVCPAN 172

Qy 178 WTAGAK 183
: : :
Db 173 WRSGER 178

RESULT 31
US-09-598-419-65
; Sequence 65, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598.419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 65
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-598-419-65

Query Match 16.5%; Score 196.5; DB 4; Length 195;
Best Local Similarity 29.6%; Pred. No. 7.5e-15;
Matches 55; Conservative 37; Mismatches 75; Indels 19; Gaps 8;

Qy 5 LGDSFPDQAEAL--GAE-HFRLHEYLGDGVMFHPNDFTPVCTTEL-AEAVKLQDSF 60
: ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 5 VGRQAPDFSGKAVVCGEKEISLADFRG-KYVVLFFYPKDFTYVCPTELHAFQDRLDV-F 62

Qy 61 TKNCKLVGSCNDLQSHREW---AKDIMAYAGSGNLPPLVCDPNRELAASLGIMDPA 117
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 EHGAVVLGCVDDIETHSRWLTWARD---AGGIEGTEYPLLADPSFKISEAFGLNPE 118

Qy 118 EKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPVD 177
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 GS-----LALRATFLIDKHGVIHAVINDPLGRSIDELRLDLSLIPFENHGMVCPAN 172

Qy 178 WTAGAK 183
: : :
Db 173 WRSGER 178

RESULT 32
US-09-556-877-294
; Sequence 294, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556.877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
```

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Db 5 VGRQAPDFSGKAVVCGEKEISLADFRG-KYVVLFFYPKDFTYVCPTELHAFQDRLDV-F 62
Qy 61 TKNCKLVGSCNDLQSHREW---AKDIMAYAGSGNLPPLVCDPNRELAASLGIMDPA 117
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 EHGAVVLGCVDDIETHSRWLTWARD---AGGIEGTEYPLLADPSFKISEAFGLNPE 118
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 118 EKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPVD 177
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 GS-----LALRATFLIDKHGVIHAVINDPLGRSIDELRLDLSLIPFENHGMVCPAN 172
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 178 WTAGAK 183
: : :
Db 173 WRSGER 178
```

```
RESULT 31
US-09-598-419-65
; Sequence 65, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598.419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 65
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-598-419-65
```

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Query Match 16.5%; Score 196.5; DB 4; Length 195;
Best Local Similarity 29.6%; Pred. No. 7.5e-15;
Matches 55; Conservative 37; Mismatches 75; Indels 19; Gaps 8;

Qy 5 LGDSFPDQAEAL--GAE-HFRLHEYLGDGVMFHPNDFTPVCTTEL-AEAVKLQDSF 60
: ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 5 VGRQAPDFSGKAVVCGEKEISLADFRG-KYVVLFFYPKDFTYVCPTELHAFQDRLDV-F 62

Qy 61 TKNCKLVGSCNDLQSHREW---AKDIMAYAGSGNLPPLVCDPNRELAASLGIMDPA 117
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 EHGAVVLGCVDDIETHSRWLTWARD---AGGIEGTEYPLLADPSFKISEAFGLNPE 118
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 118 EKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPVD 177
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 GS-----LALRATFLIDKHGVIHAVINDPLGRSIDELRLDLSLIPFENHGMVCPAN 172
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 178 WTAGAK 183
: : :
Db 173 WRSGER 178
```

```
RESULT 32
US-09-556-877-294
; Sequence 294, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556.877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
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```
Qy 178 WTAGAK 183
Db 180 WRSGER 185

RESULT 36
US-09-620-412C-92
; Sequence 92, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 92
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Chlamydia
US-09-620-412C-92

Query Match 16.5%; Score 196.5; DB 4; Length 202;
Best Local Similarity 29.6%; Pred. No. 7.9e-15;
Matches 55; Conservative 37; Mismatches 75; Indels 19; Gaps 8;

Qy 5 LGDSFPDFOAEAL--GAE-HFRLHEYLGDWGMFHPNDFTPVCTTEL-AEAVKLODSF 60
Db 12 VGRQAPDFSGKAVVCGEKEISLADFRG-KYVVLFFYPKDFTYVCPTELHAFQDRLVD-F 69

Qy 61 TTKNCKLVGFSNCNDLQSHREW---AKDIMAYAGRSNLPPLVCDPNRELAASLIGMDPA 117
Db 70 EEHGAVVLGCVSDDIETHSRWLTWARD---AGGIEGTEYPLLDSPFKISEAFGLNPE 125

Qy 118 EKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPVD 177
Db 126 GS-----LALRATFLIDKHGVRHAVINDPLGRSIDELRLDLSLIFPENHGMVCPAN 179

Qy 178 WTAGAK 183
Db 180 WRSGER 185

RESULT 37
US-09-410-568-92
; Sequence 92, Application US/09410568
; Patent No. 6555115
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fang, Hang
; APPLICANT: Jen, Shyian
; APPLICANT: Stromberg, Erica Jean
; APPLICANT: Enghart, Susan E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C2
; CURRENT APPLICATION NUMBER: US/09/410,568
; CURRENT FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 92
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Chlamydia
US-09-410-568-92

Query Match 16.5%; Score 196.5; DB 4; Length 202;
Best Local Similarity 29.6%; Pred. No. 7.9e-15;
Matches 55; Conservative 37; Mismatches 75; Indels 19; Gaps 8;

Qy 5 LGDSFPDFOAEAL--GAE-HFRLHEYLGDWGMFHPNDFTPVCTTEL-AEAVKLODSF 60
Db 12 VGRQAPDFSGKAVVCGEKEISLADFRG-KYVVLFFYPKDFTYVCPTELHAFQDRLVD-F 69

Qy 61 TTKNCKLVGFSNCNDLQSHREW---AKDIMAYAGRSNLPPLVCDPNRELAASLIGMDPA 117
Db 70 EEHGAVVLGCVSDDIETHSRWLTWARD---AGGIEGTEYPLLDSPFKISEAFGLNPE 125

Qy 118 EKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPVD 177
Db 126 GS-----LALRATFLIDKHGVRHAVINDPLGRSIDELRLDLSLIFPENHGMVCPAN 179

Qy 178 WTAGAK 183
Db 180 WRSGER 185

RESULT 38
US-09-598-419-92
; Sequence 92, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 92
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Chlamydia
US-09-598-419-92

Query Match 16.5%; Score 196.5; DB 4; Length 202;
Best Local Similarity 29.6%; Pred. No. 7.9e-15;
Matches 55; Conservative 37; Mismatches 75; Indels 19; Gaps 8;

Qy 5 LGDSFPDFOAEAL--GAE-HFRLHEYLGDWGMFHPNDFTPVCTTEL-AEAVKLODSF 60
Db 12 VGRQAPDFSGKAVVCGEKEISLADFRG-KYVVLFFYPKDFTYVCPTELHAFQDRLVD-F 69

Qy 61 TTKNCKLVGFSNCNDLQSHREW---AKDIMAYAGRSNLPPLVCDPNRELAASLIGMDPA 117
Db 70 EEHGAVVLGCVSDDIETHSRWLTWARD---AGGIEGTEYPLLDSPFKISEAFGLNPE 125

Qy 118 EKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPVD 177
Db 126 GS-----LALRATFLIDKHGVRHAVINDPLGRSIDELRLDLSLIFPENHGMVCPAN 179

Qy 178 WTAGAK 183
Db 180 WRSGER 185

RESULT 39
US-08-311-731A-84
; Sequence 84, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
```

```
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: MYCOBACTERIUM LEPRAE
;
US-08-311-731A-84

Query Match 16.2%; Score 193.5; DB 4; Length 195;
Best Local Similarity 28.3%; Pred. No. 1.7e-14;
Matches 51; Conservative 35; Mismatches 63; Indels 31; Gaps 6;

QY 3 LNLGDSFPDFQAEAL-GAEHFRLLH-EYLGD-----SWGYMFSHNDFTPVCTT 48
Db 4 LSTGQQFPAYQLTALIGDLSKVDAAQQPGDYFTTVSSDSHPGKMRVYVFPMPKDFTCPT 63
QY 49 ELAEAVKLDQSFCKKNCVLGFCSCNDLQSHREWA---KDIMAYAGRSGLNPFLPVLCDPNR 105
Db 64 EIAAFGLNEEFEGRGNAQLIGVSDSEFVHFQWRAGHEDLK-----RLPFPMLSDIKR 116
QY 106 ELAASIGIMDPAEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAELRLVLDLSQ 165
Db 117 DVSAASGALNAD-----GVADRVTFIVDPDNDIQFVSVTAGSVGRNVEEVLRLDLDALQ 169

RESULT 40
US-09-438-185A-780
; Sequence 780, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kaiman, Sue
; APPLICANT: Davis, Ronald
; TITLE OF INVENTION: Chlamydia pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 780
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
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; FEATURE:
; OTHER INFORMATION: CPr0778
US-09-438-185A-780

Query Match 16.2%; Score 193; DB 4; Length 231;
Best Local Similarity 28.0%; Pred. No. 2.5e-14;
Matches 59; Conservative 36; Mismatches 90; Indels 26; Gaps 7;

QY 1 MPLNL-GDSFPDFQAEA-LGAE--HFRLEHYLGDSGVMFSPNDFTPVCTTTELAEAVKL 56
Db 36 MTLSLVGKEAPDFVAQVNGETCTVSLKDYLG-KYVVLFFYPKDFTYVCPTELHAFQDA 94
QY 57 QDSFTKKCKLVGFCSCNDLQSHREWAKDIMAYAGRSGLNPFLPVLCDPNRELAASLGIMDP 116
Db 95 LGFHTRGAEVIGCSVDDIATHQQWLATKKKQGIEG-ITYPLLSDEDKVIGRSYHVLKP 153
QY 117 AEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAELRLVLDLSLQTAKFPPVATPV 176
Db 154 EEE-----LSFRGVFLIDKGGIIRHLVVNDLPLGRSIEBELRTLDALIFFETNGLVCPA 207
QY 177 DWTAGAKCCVVPNLAAEEAQRLLPKGHEALQ 207
Db 208 NW-----HEGERAMAPNEEGLQ 224

Search completed: October 28, 2005, 21:54:24
Job time : 47 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2005, 21:31:58 ; Search time 174 Seconds
(without alignments)

656.285 Million cell updates/sec

Title: US-10-723-123-3

Perfect score: 1194

Sequence: 1 MPLNLGDSFPDFOAEALGAE.....EALQLPSGKPYLRLTPDP 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	707	59.2	224	Q962X0	Q962X0 toxoplasma
2	668.5	56.0	223	PDX6 RAT	O35244 r peroxired
3	652.5	54.6	223	PDX6 BOVIN	O77834 b peroxired
4	645.5	54.1	224	O9TSX9	O9TSX9 sus scrofa
5	644	53.9	220	O7RGR1	O7RGR1 plasmodium
6	644	53.9	220	O86SB3	O86SB3 plasmodium
7	640.5	53.6	227	O6A0D0	O6A0D0 mus musculus
8	639.5	53.6	235	O9USA0	O9USA0 brugia mala
9	639.5	53.6	223	PDX6 MOUSE	O08709 mus musculus
10	637.5	53.4	223	PDX6 HUMAN	P30041 h peroxired
11	636	53.3	220	O8IAM2	O8IAM2 plasmodium
12	636	53.3	220	O9XXW9	O9XXW9 plasmodium
13	634	53.1	222	O6PRK9	O6PRK9 brachydanio
14	628	52.6	224	O7SYT1	O7SYT1 xenopus lae
15	625.5	52.4	217	O9USAI	O9USAI suberites d
16	621	52.0	224	O6P624	O6P624 xenopus tro
17	621	52.0	224	O7SYQ4	O7SYQ4 xenopus lae
18	619.5	51.9	219	O8MUT9	O8MUT9 aplysia cal
19	619	51.8	221	O9SWZ7	O9SWZ7 ixodes scap
20	618.5	51.8	235	O9USAI	O9USAI dirofilaria
21	617.5	51.7	235	1CPX DIRIM	O17433 dirofilaria
22	609.5	51.0	222	O9GVJ5	O9GVJ5 haemaphysal
23	607.5	50.9	224	O8BG37	O8BG37 m mus muscu
24	599	50.2	222	O694A9	O694A9 glossina mo
25	599	50.2	232	1 TSA_ONCVO	P52570 onchocerca
26	595.5	49.9	249	O7QIQ4	O7QIQ4 anopheles g
27	588	49.2	222	O9GPQ2	O9GPQ2 drosophila
28	588	49.2	222	O9VQI7	O9VQI7 drosophila
29	587	49.2	222	O95SB0	O95SB0 drosophila
30	575	48.2	216	O9GVS3	O9GVS3 plasmodium
31	572.5	47.9	219	O9SP12	O9SP12 fagopyrum e

32 521.5 43.7 248 2 Q7PZB4 Q7PZB4 anopheles g
33 517.5 43.3 220 2 Q8GVH0 Q8GVH0 oryza sativ
34 514.5 43.1 220 2 Q8GVG9 Q8GVG9 oryza sativ
35 513.5 43.0 219 2 Q8S3K4 Q8S3K4 xerophyta v
36 509 42.6 218 2 Q6E2Z6 Q6E2Z6 medicago tr
37 508.5 42.6 220 1 REHY ORYSA P52573 oryza sativ
38 503 42.1 211 2 Q8DQ04 Q8DQ04 synchococc
39 502.5 42.1 220 2 Q694A7 Q694A7 glossina mo
40 501.5 42.0 220 2 O9GPQ1 O9GPQ1 drosophila
41 501.5 42.0 220 2 O9V5K7 O9V5K7 drosophila
42 501.5 42.0 231 2 Q8MXT1 Q8MXT1 caenorhabdi
43 500 41.9 218 2 Q6W8Q2 Q6W8Q2 triticum ae
44 499 41.8 226 2 Q6BLY9 Q6BLY9 debaryomyce
45 498.5 41.8 220 2 Q9GPQ0 Q9GPQ0 drosophila

ALIGNMENTS

RESULT 1

Q962X0 PRELIMINARY; PRT; 224 AA.
AC Q962X0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Peroxidoxin 2.
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Toxoplasma.
OX NCBI_TaxID=5811;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RH;
RA Ding M., Soldati D.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397213; AAK77610.1; -;
DR HSSP; P30041; 1PRX.
DR InterPro; IPR000866; AhpC-TSA.
DR Pfam; PF00578; AhpC-TSA; 1.
SQ SEQUENCE 224 AA; 24462 MW; 16F1A05842DBED5C CRC64;

Query Match 59.2%; Score 707; DB 2; Length 224;
Best Local Similarity 57.0%; Pred. No. 4e-58;
Matches 126; Conservative 36; Mismatches 57; Indels 2; Gaps 1;
QY 3 LNLGDSFPDFOAEALG--AEHFLHBYLGDWGMFSEHPNDFTPVCTTELAEAVKLQDSF 60
DB 2 LVLGSTFPDVAHDSAGVPGDKIKLYDFLGSWGLMSHPHDFTPVCTTELAQAARMAPEF 61
QY 61 TTKNCKLVGFSNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPAEKD 120
DB 62 AKRNCKLIGFSCDDVSSHKGWAKDVMVSKLSGDLFPPIADPERKLTATDLGIMDPEEKD 121
QY 121 KKGFLPTCTCVFFISPEKKLAASILYPATTGRNFABILRVLDLSQITAKFPVATPVDDWTA 180
DB 122 KAGIPVTCRAAIYIGPDRRVKGLILYPATVGRNFKVLRALDALQLAEPVATPEGWFP 181
QY 181 GAKCCVVPNLAAEAAORLLPKGHEALQLPSGKPYLRLTPDP 221
DB 182 GDKVMVQPTLTDEAKALPKGFKEKCEPSGKNYLRYPDP 222

RESULT 2

PDX6_RAT STANDARD; PRT; 223 AA.
AC PDX6_RAT;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Peroxiredoxin 6 (EC 1.11.1.1-) (Antioxidant protein 2) (1-Cys
DE peroxiredoxin) (1-Cys PRX) (Acidic calcium-independent phospholipase
DE A2) (EC 3.1.1.1-) (aiPLA2) (Non-selenium glutathione peroxidase)

DE (EC 1.11.1.7) (NSGPx) (Thiol-specific antioxidant protein).
GN Name=Prdx6; Synonyms=Alpa2, Aop2, Tsa;
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Lung;
RA Kim T.-S., Feinstein S.I., Dodia C., Hennigan B.B., Fisher A.B.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=olfactory epithelium;
RA Andreeva S.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE OF 25-41 AND 145-162;
RX MEDLINE=97153037; PubMed=8999971; DOI=10.1074/jbc.272.4.2542;
RA Kim T.-S., Sundaresh C.S., Feinstein S.I., Dodia C., Skach W.R.,
RA Jain M.K., Nagase T., Seki N., Ishikawa K.-I., Nomura N., Fisher A.B.;
RL J. Biol. Chem. 272:10981-10981(1997).
CC -1- FUNCTION: Involved in redox regulation of the cell. Can reduce
CC H₂O(2) and short chain organic, fatty acid, and phospholipid
CC hydroperoxides. May play a role in the regulation of phospholipid
CC turnover as well as in protection against oxidative injury.
CC -1- CATALYTIC ACTIVITY: Donor + H₂O(2) = oxidized donor + 2 H₂O.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic, lysosomal and also found in
CC lung secretory organelles.
CC -1- MISCELLANEOUS: The active site is the redox-active Cys-46 oxidized
CC to Cys-SOH. Cys-SOH may rapidly react with a Cys-SH of the other
CC subunit to form an intermolecular disulfide with a concomitant
CC homodimer formation. The enzyme may be subsequently regenerated by
CC reduction of the disulfide by thioredoxin (By similarity).
CC -1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-46
CC (to Cys-SO₃H) upon oxidative stress (By similarity).
CC -1- SIMILARITY: Belongs to the AhpC/TSA family. Redoxin subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; AF014009; AAB66341.1; .
CC EMBL; Y17295; CAA76732.1; .
CC HSSP; P30041; 1PRX.
CC RGD; 71005; Prdx6.
CC InterPro; IPR000866; AhpC-TSA.
CC Pfam; PF00578; AhpC-TSA; 1.
CC Antioxidant; Direct protein sequencing; Hydrolase; Lipid degradation;
CC Lysosome; Multifunctional enzyme; Oxidoreductase; Peroxidase;
CC Redox-active center.
CC INIT_MTE 0 0 By similarity.
CC ACT_SITE 31 31 Phospholipase (By similarity).
CC ACT_SITE 46 46 Cysteine sulfenic acid (-SOH).
CC FT DISULFID 46 46 Intermediary (By similarity).
CC FT INTRACHAIN (in linked form) (By similarity).
CC SEQUENCE 223 AA; 24687 MW; E47E8537C975BF99 CRC64;
Query Match 56.08; Score 668.5; DB 1; Length 223;

Best Local Similarity 58.1%; Pred. No. 1.7e-54;
Matches 129; Conservative 29; Mismatches 59; Indels 5; Gaps 3;
QY 3 LNLGDSFPDQAE-ALGAEHFRHLHEYLGDGWSGVMFSDHNDFTPVCTTELAELAVKLODSFT 61
DB 4 LLLGDEAPNFEANTIG--HIRFHDGLGDSWGLFSHPDRDFTPVCTTELGRAKLAPEFA 61
QY 62 KKNCKLVGFSNDLQSHREWAKDIWYAGR--SGNLPPFLVCDPNRELAAASLGIMDPAEK 119
DB 62 KKNVLIALLSIDSVEDHFAWSKDINAYGAAPTEKLPFFIIDDKORDLAILLGMLDPAEK 121
QY 120 DKKGPLTCTRCVFFISPEKKLAASILYPATTGTFNFAEILRLVDSLOLTAKFPVATPDWT 179
DB 122 DEKGMPVTARVVFIQPDKKLSILYPATTGTFNFAEILRLVDSLOLTAKFPVATPDWT 181
QY 180 AGAKCCVNPALAAEEAQRLLPKGHEALQPSGKPYLRLTDPD 221
DB 182 KGESVNVLTLPPEEAKQLFPKGVFTKELPSGKKYLRYTQP 223
RESULT 3
ID_PDX6_BOVIN STANDARD; PRT; 223 AA.
AC 077854;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Peroxiredoxin 6 (EC 1.11.1.-) (Antioxidant protein 2) (1-Cys
DE peroxiredoxin) (1-Cys PRX) (Acidic calcium-independent phospholipase
DE A2) (EC 3.1.1.-) (aPLA2) (Non-selenium glutathione peroxidase)
DE (EC 1.11.1.7) (NSGPx) (PHGPx) (Ciliary body glutathione peroxidase).
GN Name=PRDX6; Synonyms=AOP2, GPX, PHGPx;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ocular ciliary body;
RX MEDLINE=98421546; PubMed=9748299; DOI=10.1074/jbc.273.40.26171;
RA Singh A.K., Shichi H.;
RT "A novel glutathione peroxidase in bovine eye. Sequence analysis, mRNA
RT level, and translation."
RL J. Biol. Chem. 273:26171-26178 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=99340074; PubMed=10409692; DOI=10.1074/jbc.274.30.21326;
RA Fisher A.B., Dodia C., Manevich Y., Chen J.-W., Feinstein S.I.;
RT "Phospholipid hydroperoxides are substrates for non-selenium
RT glutathione peroxidase."
RJ J. Biol. Chem. 274:21326-21334 (1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Oviduct;
RA Rojas Garcia P.P., Einspanier R.;
RT "Glutathione peroxidase in the bovine oviduct."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-29.
RX MEDLINE=90323120; PubMed=2373154; DOI=10.1016/0014-4835(90)90040-2;
RA Shichi H., Demar J.C.;
RT "Non-selenium glutathione peroxidase without glutathione S-transferase
RT activity from bovine ciliary body."
RL Exp. Eye Res. 50:513-520 (1990).
CC -1- FUNCTION: Involved in redox regulation of the cell. Can reduce
CC H₂O(2) and short chain organic, fatty acid, and phospholipid
CC hydroperoxides. May play a role in the regulation of phospholipid
CC turnover as well as in protection against oxidative injury.
CC -1- CATALYTIC ACTIVITY: Donor + H₂O(2) = oxidized donor + 2 H₂O.
CC -1- SUBUNIT: Homotetramer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic, lysosomal and also found in

CC -!- SIMILARITY: Belongs to the ahpC/TSA family. Rehydrin subfamily.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
CC or send an email to license@isb-sib.ch).

DR EMRY: AFOA0228: AAC63016 1: -

ВК ЕМБД; АР090194; ААС04043.1; -.
 ДН ПУМЭ АТ012010 АР04000.

DR HSSP; P30041; 1PRX.

DR Pfam; PF00578; AhpC-TSA; 1.

lysosome: Multifunctional organelle. Oxidoreductases. Peroxidases.

NW REUX-active center.

FT	ACT_SITE	31	31	Phospholipase (By similarity).

FT intermediate (Bv similarity).

similarity)

3Q SEQUENCE 223 AA; 24933 MW; 4A2C89AC1E9AF01E CRC64;

Query Match 54.6%; Score 652.5; DB 1; Length 223;

Matches	126	Conservative	30	Mismatches	61	Indels	5	Gaps	3
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3 1.NTJGNSFDDNOAE-ATGAEHETI HEVT.GDSWCIIMPESUPNDNEBIVCTETP A EAIWT ODSERT 61

[illegible]

1. $\frac{1}{2}$ 2. $\frac{1}{3}$ 3. $\frac{1}{4}$ 4. $\frac{1}{5}$ 5. $\frac{1}{6}$ 6. $\frac{1}{7}$ 7. $\frac{1}{8}$ 8. $\frac{1}{9}$ 9. $\frac{1}{10}$ 10. $\frac{1}{11}$ 11. $\frac{1}{12}$ 12. $\frac{1}{13}$ 13. $\frac{1}{14}$ 14. $\frac{1}{15}$ 15. $\frac{1}{16}$ 16. $\frac{1}{17}$ 17. $\frac{1}{18}$ 18. $\frac{1}{19}$ 19. $\frac{1}{20}$ 20. $\frac{1}{21}$ 21. $\frac{1}{22}$ 22. $\frac{1}{23}$ 23. $\frac{1}{24}$ 24. $\frac{1}{25}$ 25. $\frac{1}{26}$ 26. $\frac{1}{27}$ 27. $\frac{1}{28}$ 28. $\frac{1}{29}$ 29. $\frac{1}{30}$ 30. $\frac{1}{31}$ 31. $\frac{1}{32}$ 32. $\frac{1}{33}$ 33. $\frac{1}{34}$ 34. $\frac{1}{35}$ 35. $\frac{1}{36}$ 36. $\frac{1}{37}$ 37. $\frac{1}{38}$ 38. $\frac{1}{39}$ 39. $\frac{1}{40}$ 40. $\frac{1}{41}$ 41. $\frac{1}{42}$ 42. $\frac{1}{43}$ 43. $\frac{1}{44}$ 44. $\frac{1}{45}$ 45. $\frac{1}{46}$ 46. $\frac{1}{47}$ 47. $\frac{1}{48}$ 48. $\frac{1}{49}$ 49. $\frac{1}{50}$ 50. $\frac{1}{51}$ 51. $\frac{1}{52}$ 52. $\frac{1}{53}$ 53. $\frac{1}{54}$ 54. $\frac{1}{55}$ 55. $\frac{1}{56}$ 56. $\frac{1}{57}$ 57. $\frac{1}{58}$ 58. $\frac{1}{59}$ 59. $\frac{1}{60}$ 60. $\frac{1}{61}$ 61. $\frac{1}{62}$ 62. $\frac{1}{63}$ 63. $\frac{1}{64}$ 64. $\frac{1}{65}$ 65. $\frac{1}{66}$ 66. $\frac{1}{67}$ 67. $\frac{1}{68}$ 68. $\frac{1}{69}$ 69. $\frac{1}{70}$ 70. $\frac{1}{71}$ 71. $\frac{1}{72}$ 72. $\frac{1}{73}$ 73. $\frac{1}{74}$ 74. $\frac{1}{75}$ 75. $\frac{1}{76}$ 76. $\frac{1}{77}$ 77. $\frac{1}{78}$ 78. $\frac{1}{79}$ 79. $\frac{1}{80}$ 80. $\frac{1}{81}$ 81. $\frac{1}{82}$ 82. $\frac{1}{83}$ 83. $\frac{1}{84}$ 84. $\frac{1}{85}$ 85. $\frac{1}{86}$ 86. $\frac{1}{87}$ 87. $\frac{1}{88}$ 88. $\frac{1}{89}$ 89. $\frac{1}{90}$ 90. $\frac{1}{91}$ 91. $\frac{1}{92}$ 92. $\frac{1}{93}$ 93. $\frac{1}{94}$ 94. $\frac{1}{95}$ 95. $\frac{1}{96}$ 96. $\frac{1}{97}$ 97. $\frac{1}{98}$ 98. $\frac{1}{99}$ 99. $\frac{1}{100}$ 100. $\frac{1}{101}$ 101. $\frac{1}{102}$ 102. $\frac{1}{103}$ 103. $\frac{1}{104}$ 104. $\frac{1}{105}$ 105. $\frac{1}{106}$ 106. $\frac{1}{107}$ 107. $\frac{1}{108}$ 108. $\frac{1}{109}$ 109. $\frac{1}{110}$ 110. $\frac{1}{111}$ 111. $\frac{1}{112}$ 112. $\frac{1}{113}$ 113. $\frac{1}{114}$ 114. $\frac{1}{115}$ 115. $\frac{1}{116}$ 116. $\frac{1}{117}$ 117. $\frac{1}{118}$ 118. $\frac{1}{119}$ 119. $\frac{1}{120}$ 120. $\frac{1}{121}$ 121. $\frac{1}{122}$ 122. $\frac{1}{123}$ 123. $\frac{1}{124}$ 124. $\frac{1}{125}$ 125. $\frac{1}{126}$ 126. $\frac{1}{127}$ 127. $\frac{1}{128}$ 128. $\frac{1}{129}$ 129. $\frac{1}{130}$ 130. $\frac{1}{131}$ 131. $\frac{1}{132}$ 132. $\frac{1}{133}$ 133. $\frac{1}{134}$ 134. $\frac{1}{135}$ 135. $\frac{1}{136}$ 136. $\frac{1}{137}$ 137. $\frac{1}{138}$ 138. $\frac{1}{139}$ 139. $\frac{1}{140}$ 140. $\frac{1}{141}$ 141. $\frac{1}{142}$ 142. $\frac{1}{143}$ 143. $\frac{1}{144}$ 144. $\frac{1}{145}$ 145. $\frac{1}{146}$ 146. $\frac{1}{147}$ 147. $\frac{1}{148}$ 148. $\frac{1}{149}$ 149. $\frac{1}{150}$ 150. $\frac{1}{151}$ 151. $\frac{1}{152}$ 152. $\frac{1}{153}$ 153. $\frac{1}{154}$ 154. $\frac{1}{155}$ 155. $\frac{1}{156}$ 156. $\frac{1}{157}$ 157. $\frac{1}{158}$ 158. $\frac{1}{159}$ 159. $\frac{1}{160}$ 160. $\frac{1}{161}$ 161. $\frac{1}{162}$ 162. $\frac{1}{163}$ 163. $\frac{1}{164}$ 164. $\frac{1}{165}$ 165. $\frac{1}{166}$ 166. $\frac{1}{167}$ 167. $\frac{1}{168}$ 168. $\frac{1}{169}$ 169. $\frac{1}{170}$ 170. $\frac{1}{171}$ 171. $\frac{1}{172}$ 172. $\frac{1}{173}$ 173. $\frac{1}{174}$ 174. $\frac{1}{175}$ 175. $\frac{1}{176}$ 176. $\frac{1}{177}$ 177. $\frac{1}{178}$ 178. $\frac{1}{179}$ 179. $\frac{1}{180}$ 180. $\frac{1}{181}$ 181. $\frac{1}{182}$ 182. $\frac{1}{183}$ 183. $\frac{1}{184}$ 184. $\frac{1}{185}$ 185. $\frac{1}{186}$ 186. $\frac{1}{187}$ 187. $\frac{1}{188}$ 188. $\frac{1}{189}$ 189. $\frac{1}{190}$ 190. $\frac{1}{191}$ 191. $\frac{1}{192}$ 192. $\frac{1}{193}$ 193. $\frac{1}{194}$ 194. $\frac{1}{195}$ 195. $\frac{1}{196}$ 196. $\frac{1}{197}$ 197. $\frac{1}{198}$ 198. $\frac{1}{199}$ 199. $\frac{1}{200}$ 200. $\frac{1}{201}$ 201. $\frac{1}{202}$ 202. $\frac{1}{203}$ 203. $\frac{1}{204}$ 204. $\frac{1}{205}$ 205. $\frac{1}{206}$ 206. $\frac{1}{207}$ 207. $\frac{1}{208}$ 208. $\frac{1}{209}$ 209. $\frac{1}{210}$ 210. $\frac{1}{211}$ 211. $\frac{1}{212}$ 212. $\frac{1}{213}$ 213. $\frac{1}{214}$ 214. $\frac{1}{215}$ 215. $\frac{1}{216}$ 216. $\frac{1}{217}$ 217. $\frac{1}{218}$ 218. $\frac{1}{219}$ 219. $\frac{1}{220}$ 220. $\frac{1}{221}$ 221. $\frac{1}{222}$ 222. $\frac{1}{223}$ 223. $\frac{1}{224}$ 224. $\frac{1}{225}$ 225. $\frac{1}{226}$ 226. $\frac{1}{227}$ 227. $\frac{1}{228}$ 228. $\frac{1}{229}$ 229. $\frac{1}{230}$ 230. $\frac{1}{231}$ 231. $\frac{1}{232}$ 232. $\frac{1}{233}$ 233. $\frac{1}{234}$ 234. $\frac{1}{235}$ 235. $\frac{1}{236}$ 236. $\frac{1}{237}$ 237. $\frac{1}{238}$ 238. $\frac{1}{239}$ 239. $\frac{1}{240}$ 240

121 1234567891011121314151617181920212223242526272829303132333435363738394041424344454647484950515253545556575859606162636465666768697071727374757677787980818283848586878889909192939495969798991001011021031041051061071081091101111121131141151161171181191201211221231241251261271281291301311321331341351361371381391401411421431441451461471481491501511521531541551561571581591601611621631641651661671681691701711721731741751761771781791801811821831841851861871881891901911921931941951961971981992002012022032042052062072082092102112122132142152162172182192202212222232242252262272282292302312322332342352362372382392402412422432442452462472482492502512522532542552562572582592602612622632642652662672682692702712722732742752762772782792802812822832842852862872882892902912922932942952962972982993003013023033043053063073083093103113123133143153163173183193203213223233243253263273283293303313323333343353363373383393403413423433443453463473483493503513523533543553563573583593603613623633643653663673683693703713723733743753763773783793803813823833843853863873883893903913923933943953963973983994004014024034044054064074084094104114124134144154164174184194204214224234244254264274284294304314324334344354364374384394404414424434444454464474484494504514524534544554564574584594604614624634644654664674684694704714724734744754764774784794804814824834844854864874884894904914924934944954964974984995005015025035045055065075085095105115125135145155165175185195205215225235245255265275285295305315325335345355365375385395405415425435445455465475485495505515525535545555565575585595605615625635645655665675685695705715725735745755765775785795805815825835845855865875885895905915925935945955965975985996006016026036046056066076086096106116126136146156166176186196206216226236246256266276286296306316326336346356366376386396406416426436446456466476486496506516526536546556566576586596606616626636646656666676686696706716726736746756766776786796806816826836846856866876886896906916926936946956966976986997007017027037047057067077087097107117127137147157167177187197207217227237247257267277287297307317327337347357367377387397407417427437447457467477487497507517527537547557567577587597607617627637647657667677687697707717727737747757767777787797807817827837847857867877887897907917927937947957967977987998008018028038048058068078088098108118128138148158168178188198208218228238248258268278288298308318328338348358368378388398408418428438448458468478488498508518528538548558568578588598608618628638648658668678688698708718728738748758768778788798808818828838848858868878888898908918928938948958968978988999009019029039049059069079089099109119129139149159169179189199209219229239249259269279289299309319329339349359369379389399409419429439449459469479489499509519529539549559569579589599609619629639649659669679689699709719729739749759769779789799809819829839849859869879889899909919929939949959969979989991000100110021003100410051006100710081009101010111012101310141015101610171018101910201021102210231024102510261027102810291030103110321033103410351036103710381039104010411042104310441045104610471048104910501051105210531054105510561057105810591060106110621063106410651066106710681069107010711072107310741075107610771078107910801081108210831084108510861087108810891090109110921093109410951096109710981099110011011102110311041105110611071108110911101111111211131114111511161117111811191120112111221123112411251126112711281129113011311132113311341135113611371138113911401141114211431144114511461147114811491150115111521153115411551156115711581159116011611162116311641165116611671168116911701171117211731174117511761177117811791180118111821183118411851186118711881189119011911192119311941195119611971198119912001201120212031204120512061207120812091210121112121213121412151216121712181219122012211222122312241225122612271228122912301231123212331234123512361237123812391240124112421243124412451246124712481249125012511252125312541255125612571258125912601261126212631264126512661267126812691270127112721273127412751276127712781279128012811282128312841285128612871288128912901291129212931294129512961297129812991

QY 120 DKRGLPLTCRCVFFISPEKKLAASILYPATIGRNFAEILRVLDLSQLTAKFPVATPVDWT 179

db 122 DEKGMPVTARVVFIFGPDKKLSILYPATTGRNFDEILRVIISLQLTAEKRVATPVDWK 181

180 AGAKCCWVPNTAAREAOPI.T.PKCHET.I.T.PSGKPV.I.PI.TPDP 221

[illegible]

RESULT 4

ID 09TSX9 PRELIMINARY; PRT. 224 AA

01-MAY-2000 (M-FRI) 13 C00040)

01-MAY-2000 (TREMBlérel. 13, Last sequence update)

DE Non-selenium glutathione phospholipid hydroperoxide peroxidase

GN Name=phopx:

Das verlorene (1997):
 Einkehrworte: Motzen: Obendate: Quantitate: Einkehrworte:
 Einkehrworte: Quantitate: Obendate: Einkehrworte:

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

RN [1]

RC TISSUE=Oviduct:

Qy 64 NCKLVGFSNDLQSHREWAKDIMAYAGR-----SGN-LPPPLVCDPNRELAASLGI 113
 Db 67 NVKLGSLSDSVQSHRWADDIIEELCRMKSGDSNCTCCGNKLPPIIADNDRSLASKLM 126
 Qy 114 MDPRAKDKGLPLTRCVRFFISPPKLAAILYPATTGRNFAELRLVDSLQLTAKPPVA 173
 Db 127 MDPDECDEKGAALPARCLFIIGPEKTKLSILYPATTGRNFDLRLVDSLQLTATKLVA 186
 Qy 174 TPVDWTAGAKCVCVVPNLAABEAOBLLPKGHEALPLSGKPYLRITPDPR 222
 Db 187 TPVDWQNGDCVVPPTINDNEAKKLFGEKINTVELPSGKPYLRVWAHPK 235

RESULT 9
 PDX6 MOUSE
 ID_PDX6_MOUSE STANDARD; PRT; 223 AA.
 AC 090709; Q91WT2; Q9QWP4; Q9QWQ0;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 05-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Peroxiredoxin 6 (EC 1.11.1.-) (Antioxidant protein 2) (1-Cys
 DE Peroxiredoxin 6 (EC 1.11.1.-) (Antioxidant protein 2) (1-Cys
 DE A2) (EC 3.1.1.-) (aPLA2) (Non-selenium glutathione peroxidase)
 DE (EC 1.11.1.-) (NSGFX).
 GN Name=Pdx6; Synonyms=Aop2, Ltw4, Pdx5;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-25.
 RC STRAIN=C3H/FEJ, C57BL/6J, and DBA/2J; TISSUE=Kidney, and Liver;
 RX MEDLINE=97349116; PubMed=9205120; DOI=10.1006/geno.1997.4762;
 RA Iakubova O.A., Macella L.A., Her H., Beier D.R.;
 RT "Ltw4 protein on mouse chromosome 1 is a member of a family of
 RT antioxidant proteins";
 RL Genomics 42:474-478(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Skin;
 RX MEDLINE=97419117; PubMed=9291135;
 RA Munz B., Frank S., Huebner G., Olsen E., Werner S.;
 RT "A novel type of glutathione peroxidase: expression and regulation
 RT during wound repair";
 RL Biochem. J. 326:579-585(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ, and C57BL/6; TISSUE=Brain;
 RX MEDLINE=99326508; PubMed=10395907; DOI=10.1016/S0378-1119(99)00190-0;
 RA Lee T.-H., Yu S.-L., Kim S.-U., Kim Y.-M., Choi I., Kang S.W.,
 RA Rhee S.G., Yu D.-Y.;
 RT "Characterization of the murine gene encoding 1-Cys peroxiredoxin and
 RT identification of highly homologous genes";
 RL Gene 234:337-344(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Pituitary;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Shirlim L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numa K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RN Nature 420:563-573(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE FROM N.A.
 CC -1- FUNCTION: Involved in redox regulation of the cell. Can reduce
 CC H(2)O(2) and short chain organic, fatty acid, and phospholipid
 CC hydroperoxides. May play a role in the regulation of phospholipid
 CC turnover as well as in protection against oxidative injury (By
 CC similarity).
 CC -1- CATALYTIC ACTIVITY: Donor + H(2)O(2) = oxidized donor + 2 H(2)O.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic, lysosomal and also found in
 CC lung secretory organelles (By similarity).
 CC -1- TISSUE SPECIFICITY: Highly expressed in heart, kidney and liver.
 CC Moderate expression in brain and stomach. Very low levels in
 CC intestine.
 CC -1- MISCELLANEOUS: The active site is the redox-active Cys-46 oxidized
 CC to Cys-SOH. Cys-SOH may rapidly react with a Cys-SH of the other
 CC subunit to form an intermolecular disulfide with a concomitant
 CC homodimer formation. The enzyme may be subsequently regenerated by
 CC reduction of the disulfide by thioredoxin (By similarity).
 CC -1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-46
 CC (to Cys-SO3H) upon oxidative stress (By similarity).
 CC -1- SIMILARITY: Belongs to the ahpc/TSA family. Rehydrin subfamily.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF046670; AAC53377.1; -
 CC EMBL; Y12883; CA973383.1; -
 CC EMBL; AF093852; AAC63376.1; -
 CC EMBL; AF093853; AAC67553.1; -
 CC EMBL; AF093857; AAD03716.1; -
 CC EMBL; AF093854; AAD03716.1; JOINED.
 DR

DR EMBL; AF093855; AAD03716.1; JOINED.
 DR EMBL; AF093856; AAD03716.1; JOINED.
 DR EMBL; AK030413; AAC26952.1; -.
 DR EMBL; BC013489; AAC13489.1; -.
 DR HSSP; P30041; 1PRX.
 DR SWISS-2DPAGE; O08709; MOUSE.
 DR MGI; 894320; Ptdx6.
 DR InterPro; IPR000866; Ahpc-TSA.
 DR Pfam; PF00578; Ahpc-TSA; 1.
 KW Antioxidant; Direct protein sequencing; Hydrolase; Lipid degradation;
 KW Lysozyme; Multifunctional enzyme; Oxidoreductase; Peroxidase;
 KW Redox-active center.
 FT INIT_MET 0
 FT ACT_SITE 31 31 Phospholipase (By similarity).
 FT ACT_SITE 46 46 Cysteine sulfenic acid (-SOH)
 FT DISULFID 46 46 Intermediate (By similarity).
 FT VARIANT 123 123 Interchain (in linked form) (By similarity).
 FT VARIANT 123 123 D -> A (in strain C57BL/6, strain C57BL/6J and strain FVB/N).
 FT CONFLICT 153 153 G -> S (in Ref. 3; AAC67553).
 FT CONFLICT 180 180 W -> R (in Ref. 3; AAD03716).
 SQ SEQUENCE 223 AA; 24739 MW; A4F2B1E36180BBFC CRC64;
 Query Match 53.68; Score 639.5; DB 1; Length 223;
 Best Local Similarity 55.99; Pred. No. 8.8e-52;
 Matches 124; Conservative 27; Mismatches 66; Indels 5; Gaps 3;
 QY 3 LNLGDSPPDQAE-ALGAERHRLHEVLGDSWGMFSGHPNDFTVCVTELAEAVKLQDSPT 61
 DB 4 LLLGDEAPNEANTTIG--RIRPHDFLGDSWGLFSPHPRDFTVCVTELGRAKLAPEFA 61
 QY 62 KQCKLVGFCNDLQSHREWAKDIMAYAGR--SGNLPPFLVCDPNRELAASGIMDPAEK 119
 DB 62 KRNVLKIALSIDSVEDHLAWSKDINAYNGETPKLPFPPIIDKGRDLAILGLMDPVEK 121
 QY 120 DKKGLPITCRVFPISPEKLAASILVPATTGRNFAELRLVLDLSLQAKFPVATPDWT 179
 DB 122 DNNMPVTARVTFIPGPKLKLSILYPATTGRNFDILRVDSLQITGKVPATPDVK 181
 QY 180 AGAKCCVFNLAEEAQRLLPKGHEALQLPSGKPYRLRLTDP 221
 DB 182 KGESVMVPTLSSEEAQCKPKGVFTKELPSGKKYLYTPQP 223
 RESULT 10
 ID_PDX6 HUMAN
 AC P30041; P32077; STANDARD; PRT; 223 AA.
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 23-OCT-2004 (Rel. 45, Last annotation update)
 DE Peroxiredoxin 6 (EC 1.11.1.-) (Antioxidant protein 2) (1-Cys
 DE peroxiredoxin) (1-Cys PRX) (Acidic calcium-independent phospholipase
 DE A2) (EC 3.1.1.-) (aIPUA2) (Non-selenium glutathione peroxidase)
 DE (EC 1.11.1.7) (NSGPx) (24 kDa protein) (Liver 2D page spot 40) (Red
 DE blood cells page spot 12).
 GN Name=PRDX6; Synonyms=AOP2, KIAA0106;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97153037; PubMed=8999971; DOI=10.1074/jbc.272.4.2542;
 RA Kim T.-S., Sundaresh C.S., Feinstein S.I., Dodia C., Skach W.R.,
 RA Jain M.K., Nagase T., Seki N., Ishikawa K.-I., Nomura N., Fisher A.B.;
 RA "Prediction of the coding sequences of unidentified human genes. III.
 RA The coding sequences of 40 new genes (KIAA0081-KIAA0120) deduced by
 RT independent phospholipase A2 and properties of the expressed
 RT protein.";
 RL J. Biol. Chem. 272:2542-2550(1997).
 RN [2]
 RP ERRATUM.

RA Kim T.-S., Sundaresh C.S., Feinstein S.I., Dodia C., Skach W.R.,
 RA Jain M.K., Nagase T., Seki N., Ishikawa K.-I., Nomura N., Fisher A.B.;
 RL J. Biol. Chem. 272:10981-10981(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RX MEDLINE=95308325; PubMed=7788527;
 RA Nagase T., Miyajima N., Tanaka A., Sazuka T., Seki N., Sato S.,
 RA Tabata S., Ishikawa K.-I., Kawabayashi Y., Kotani H., Nomura N.;
 RT "Prediction of the coding sequences of unidentified human genes. III.
 RT The coding sequences of 40 new genes (KIAA0081-KIAA0120) deduced by
 RT analysis of cDNA clones from human cell line KG-1.";
 RL DNA Res. 2:37-43(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97203272; PubMed=9050990; DOI=10.1038/sj.onc.1200905;
 RA Frank S., Munz B., Warner S.;
 RT "The human homologue of a bovine non-selenium glutathione peroxidase
 RT is a novel keratinocyte growth factor-regulated gene.";
 RL Oncogene 14:915-921(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain, and Testis;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Murzyn D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Wahing J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwold J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE OF 1-21.
 RC TISSUE=Platelet;
 RX MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;
 RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,
 RA Thomas G.R., Vandekerckhove J.;
 RT "Exploring proteomes and analyzing protein processing by mass
 RT spectrometric identification of sorted N-terminal peptides.";
 RN Nat. Biotechnol. 21:566-569(2003).
 RP PARTIAL SEQUENCE OF 1-14.
 RC TISSUE=Liver;
 RX MEDLINE=93162045; PubMed=1286669;
 RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
 RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,
 RA Appel R.D., Hughes G.J.;
 RT "Human liver protein map: a reference database established by
 RT microsequencing and gel comparison.";
 RL Electrophoresis 13:992-1001(1992).
 RN [8]
 RP PARTIAL SEQUENCE OF 1-12.
 RC TISSUE=Erythrocyte;
 RX MEDLINE=94147970; PubMed=8313871;
 RA Golaz O., Hughes G.J., Frutiger S., Paquet N., Bairoch A.,
 RA Pasquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C.,
 RA Balant L., Hochstrasser D.F.;
 RT "Plasma and red blood cell protein maps: update 1993.";
 RL Electrophoresis 14:1223-1231(1993).
 RN [9]

RP CHARACTERIZATION, AND MUTAGENESIS.
RX MEDLINE=98165813; PubMed=9497358; DOI=10.1074/jbc.273.11.6303;
RA Kang S.W., Baines I.C., Rhee S.G.;
RT "Characterization of a mammalian peroxidoxin that contains one
RL conserved cysteine";
RN J. Biol. Chem. 273:6303-6311(1998).
[10]
RP CHARACTERIZATION, AND MUTAGENESIS.
RX MEDLINE=20435792; PubMed=10893423; DOI=10.1074/jbc.M005073200;
RA Chen J.-W., Dodia C., Feinstein S.I., Jain M.K., Fisher A.B.;
RT "1-Cys peroxidoxin, a bifunctional enzyme with glutathione
RL peroxidase and phospholipase A2 activities";
RN J. Biol. Chem. 275:28421-28427(2000).
[11]
RP OXIDATION OF CYS-46.
RX MEDLINE=22201787; PubMed=12059788; DOI=10.1042/BJ20020525;
RA Wagner E., Luche S., Penna L., Chevallet M., van Dorsselaer A.,
RL Leize-Wagner E., Rabilloud T.;
RT "A method for detection of overoxidation of cysteines: peroxidoxins
are oxidized in vivo at the active-site cysteine during oxidative
stress";
RN Biochem. J. 366:777-785(2002).
[12]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=98246415; PubMed=9587003;
RA Choi H.-J., Kang S.W., Yang C.-H., Rhee S.G., Ryu S.-E.;
RT "Crystal structure of a novel human peroxidase enzyme at 2.0-A
RL resolution";
RN Nat. Struct. Biol. 5:400-406(1998).
CC -1- FUNCTION: Involved in redox regulation of the cell. Can reduce
CC H₂O₂ and short chain organic, fatty acid, and phospholipid
CC hydroperoxides. May play a role in the regulation of phospholipid
CC turnover as well as in protection against oxidative injury.
CC -1- CATALYTIC ACTIVITY: Donor + H₂O₂ = oxidized donor + 2 H₂O.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic, lysosomal and also found in
CC lung secretory organelles (By similarity).
CC -1- MISCELLANEOUS: The active site is the redox-active Cys-46 oxidized
CC to Cys-SOH. Cys-SOH may rapidly react with a Cys-SH of the other
CC subunit to form an intermolecular disulfide with a concomitant
CC homodimer formation. The enzyme may be subsequently regenerated by
CC reduction of the disulfide by thioredoxin.
CC -1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-46
CC (to Cys-SO₃H) upon oxidative stress.
CC -1- SIMILARITY: Belongs to the AhpC/TSA family. Rehydrin subfamily.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: D14662; BAA03496.1; --
CC EMBL: BC035857; AAH35857.1; --
CC EMBL: BC035550; AAH35550.1; --
CC PDB: 1PRX; X-ray; A/B=1-223.
CC DR SWISS-2DPAGE; P30041; HUMAN.
CC OGP; P30041; --
CC DR Siena-2DPAGE; P30041; --
CC DR Geniv; HGNC:16753; PRDX6.
CC DR H-InVDB; HIX001339; --
CC DR MIM; 602316; --
CC DR GO; GO:0005829; Cytosol; NAS.
CC DR GO; GO:0016209; F:antioxidant activity; NAS.
CC DR GO; GO:0016224; F:non-selenium glutathione peroxidase activity; IDA.
CC DR GO; GO:0004623; F:phospholipase A2 activity; IDA.
CC DR GO; GO:0009395; P:phospholipid catabolism; IDA.
CC DR GO; GO:0009379; P:response to oxidative stress; IDA.
CC DR InterPro; IPR000866; AhpC-TSA.
CC DR Pfam; PF00578; AhpC-TSA; 1.
CC 3D-structure; Antioxidant; Direct protein sequencing; Hydrolase;

KW Lipid degradation; Lysosome; Multifunctional enzyme; Oxidoreductase;
KW Peroxidase; Redox-active center.
FT INIT_MET 0 0 Phospholipase.
FT ACT_SITE 31 31 Cysteine sulfenic acid (-SOH)
FT ACT_SITE 46 46 intermediate.
FT DISULFID 46 46 Interchain (in linked form) (By
FT similarity).
FT MUTAGEN 31 31 S->A: Loss of AIPLA2 activity, but no
FT effect on NSGFX activity.
FT MUTAGEN 46 46 C->S: Loss of NSGFX activity, but no
FT effect on AIPLA2 activity.

TURN 6 7
FT STRAND 9 9
FT STRAND 14 17
FT TURN 18 19
FT STRAND 20 23
FT HELIX 24 28
FT TURN 29 30
FT STRAND 32 38
FT HELIX 44 61
FT TURN 62 64
FT STRAND 65 71
FT HELIX 75 88
FT TURN 89 90
FT STRAND 101 103
FT TURN 105 106
FT HELIX 108 112

Query Match 53.4%; Score 637.5; DB 1; Length 223;
Best Local Similarity 56.6%; Pred. No. 1.4e-51;
Matches 125; Conservative 28; Mismatches 65; Indels 3; Gaps 2;
Qy 3 LNLGDSFPQAEALGAELHLEHLYGLDGSWGMFSDPTVCTTLEAAVQLQDSFTK 62
Db 4 LLLGDVAPFEANTT-VGRIRHDFLGDGSLFSDPTVCTTLEAAVQLQDSFTK 62
Qy 63 KNCVLGVGSCNDLQSHREWAKOIMAY--AGRSNLPFPLVCDPNRELAASLGIMDPAEKD 120
Db 63 RNVKLTALSIDSVEDHLAWSKOINAYNCEPTEKLPFPIDRRRELAILLGMIDPAEKD 122
Qy 121 KGLPLTCTRCVFFISPEKKLAASILYPATTGRNFALILRVLDLSQLTAKFPVATPVDMTA 180
Db 123 EKGMPVTARVVFVFGDPKKLKLILYPATTGRNFDILRVVISQLTAERKRVATPVDMKD 182
Qy 181 GAKCCVVPNLAAEEAQRLLPKGHEALQLPSGKBYLRITPDP 221
Db 183 GDSVMVLTPIPEBEAKLPFGKGVFTKELPSGKKLYRITPDP 223

RESULT 11

Q8IAM2 Q8IAM2 PRELIMINARY; PRT; 220 AA.
ID Q8IAM2
AC Q8IAM2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 1-cys peroxidoxin.
GN Names:1-cyspxn; Synonyms:PF08_0131;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
RX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,
RA Quail M., Barrell B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL844507; CAD51341.1; --
DR HSSP; P30041; 1PRX
DR InterPro; IPR000866; AhpC-TSA.
DR Pfam; PF00578; AhpC-TSA; 1.
SQ SEQUENCE 220 AA; 25164 MW; ECDA692845B8A15F CRC64;

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Query Match      53.3%; Score 636; DB 2; Length 220;
Best Local Similarity 55.9%; Pred. No. 1.8e-51;
Matches 123; Conservative 32; Mismatches 57; Indels 8; Gaps 3;

QY 1 MPLNLGDSFPDFOAEALGAEH-FRLHEYLGDSDGVNMFHSPNDFTPVCTTTELAEAVKLQDS 59
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MAYHLGATPNTATASNDVGVDFYKYVDGNWAILFSPHDPFTPVCTTTELAEFQGWHEE 60
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 60 FTKKNCKLVGFSNDLQSHREWAKDIMAYAGRSNL---PFPLVCDPNRELAASLGIMDP 116
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 FLKLNCKLIGFSCNSKESHDQWIEDIKFY----GNLDKWDIPMVCDESRELANQLKIMDE 116
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 117 AEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGNFAEILRVLDLSLOLTAKFPVATPV 176
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 117 KENDIAGLPLTCRCVFFISPDKKVKATVLYPATYTGNSQEIILRVLSLOLTNTHPVATPV 176
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 177 DWTAGAKCCVVPNLAEEAQRLLPKGHEALQPLSGKPYLR 216
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 177 NWKEGDKCCLIPSDVDNADLPKLFKNEVKKLDVFSQKAYLR 216
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 12
Q9XXW9 PRELIMINARY; PRT; 220 AA.
AC Q9XXW9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 1-cys peroxidoxin.
GN Name=1-CyPxn;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FCR-3;
RX MEDLINE=20416494; PubMed=10960175; DOI=10.1016/S0166-6851(00)00243-7;
RA Kawazu S., Tsuji N., Hatabu T., Kawai S., Matsumoto Y., Kano S.;
RT "Molecular cloning and characterization of a peroxidoredoxin from the
RT human malaria parasite Plasmodium falciparum.";
RL Mol. Biochem. Parasitol. 109:165-169 (2000).
DR EMBL; AB020595; BAA78369.1; -.
DR HSSP; P30041; IPRX.
DR InterPro; IPR000866; AhpC-TSA.
DR Pfam; PF00578; AhpC-TSA; 1.
SQ SEQUENCE 220 AA; 25164 MW; ECDA692845B8A15F CRC64;

Query Match      53.3%; Score 636; DB 2; Length 220;
Best Local Similarity 55.9%; Pred. No. 1.8e-51;
Matches 123; Conservative 32; Mismatches 57; Indels 8; Gaps 3;

QY 1 MPLNLGDSFPDFOAEALGAEH-FRLHEYLGDSDGVNMFHSPNDFTPVCTTTELAEAVKLQDS 59
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MAYHLGATPNTATASNDVGVDFYKYVDGNWAILFSPHDPFTPVCTTTELAEFQGWHEE 60
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 60 FTKKNCKLVGFSNDLQSHREWAKDIMAYAGRSNL---PFPLVCDPNRELAASLGIMDP 116
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 FLKLNCKLIGFSCNSKESHDQWIEDIKFY----GNLDKWDIPMVCDESRELANQLKIMDE 116
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 117 AEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGNFAEILRVLDLSLOLTAKFPVATPV 176
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 117 KENDIAGLPLTCRCVFFISPDKKVKATVLYPATYTGNSQEIILRVLSLOLTNTHPVATPV 176
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 177 DWTAGAKCCVVPNLAEEAQRLLPKGHEALQPLSGKPYLR 216
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 177 NWKEGDKCCLIPSDVDNADLPKLFKNEVKKLDVFSQKAYLR 216
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RESULT 13
Q6PBK9 PRELIMINARY; PRT; 222 AA.
AC Q6PBK9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

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DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Peroxiredoxin 6.
GN Name=prdx6;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wild-type; TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Maman A., Rodrigues S., Sanchez A.,
RA Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wild-type; TISSUE=Eye;
RA Director MGC Project;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC059671; AAH59671.1; -.
DR ZFIN; ZDB-GENE-040426-1778; zgc:73360.
SQ SEQUENCE 222 AA; 25009 MW; 3B4EB7196F1B0D1E CRC64;

Query Match      53.1%; Score 634; DB 2; Length 222;
Best Local Similarity 53.2%; Pred. No. 2.9e-51;
Matches 118; Conservative 43; Mismatches 55; Indels 6; Gaps 4;

QY 1 MPLNLGDSFPDFOAE-ALGAEHFRLHEYLGDSDGVNMFHSPNDFTPVCTTTELAEAVKLQD 58
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MPGILLGDVFPNFEADTTIG--KIRFHEFLGNSWGLFSPHDPFTPVCTTTELAARAKLHE 58
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 59 SFTKNCKLVGFSNDLQSHREWAKDIMAYAGRS--NLPPFLVCDPNRELAASLGIMDP 116
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 59 EFKRDVKMIALSIDSVEDHRKWSIEDILAFNQDKACCPMPFFTIADDKRELSVLLGMLDP 118
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 117 AEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGNFAEILRVLDLSLOLTAKFPVATPV 176
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 119 DERDQGMPLTARCVFVGVGPDRLKLSILYPATTGNFDEILRVLDLSLOLTATKRVATPV 178
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 177 DWTAGAKCCVVPNLAEEAQRLLPKGHEALQPLSGKPYLR 218
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 179 DWPQGVNVIPLSDEEANKLFPAGFTLKEVPSGKKYIRY 220
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 14
Q7SVT1 PRELIMINARY; PRT; 224 AA.
AC Q7SVT1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Prdx6-prov protein.
GN Name=prdx6-prov;
OS Xenopus laevis (African clawed frog).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RA Klein S., Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR ENBL; BC054278; AAH54278.1; -
 DR InterPro; IPR000866; AhpC-TSA.
 DR Pfam; PF00578; AhpC-TSA; 1.
 SQ SEQUENCE 224 AA; 25363 MW; 7CD67F59315A3CAB CRC64;
 Query Match 52.6%; Score 628; DB 2; Length 224;
 Best Local Similarity 53.1%; Pred. No. 1.1e-50;
 Matches 120; Conservative 37; Mismatches 63; Indels 6; Gaps 4;
 QY 1 MP-LNIGDSPDQAE-ALGAEHRLHYLGDSWGMFSPNDPTVCTTELAEAVKLQD 58
 Db 1 MPGLILGERPDEADTTIG--RIKFHPIGDRWGLFSPHPRDTPVCTTELGRCVKLAP 58
 QY 59 SFTKKNCKLVGFCNDLQSHREWAKDIMAY--AGRSNLPFLVCDPNRELAASLGIMDP 116
 Db 59 EFKKNVRMTALSDSVDHLGSKINSYNCDEPTETLFPPIADPKRDLAVQLGMLDP 118
 QY 117 AEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGGRNFABILRVLDLSQLTAKFPVATPV 176
 Db 119 DEKDMQMPVTPVPTPEEARKIFTCGVFTKELPSGKKLYRTPOQ 224
 QY 177 DWTAGAKCCVVPNLAAEAQRLLPKGHEALQLPSGKPYRLTDPDR 222
 Db 179 DWRPGDRVMVPTVPEEARKIFTCGVFTKELPSGKKLYRTPOQ 224
 RESULT 15
 Q966Y9
 ID Q966Y9 PRELIMINARY; PRT; 217 AA.
 AC Q966Y9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Glutathione peroxidase.
 GN Name-gpx;
 OS Suberites domuncula (Sponge).
 OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
 OC Hadromerida; Suberitidae; Suberites.
 OX NCBI_TaxID=55567;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20033590; PubMed=10564648;
 RA Kruse M., Steffen R., Batel R., Mueller I.M., Mueller W.E.G.;
 RT "Differential expression of allograft inflammatory factor 1 and of
 RT glutathione peroxidase during auto- and allograft response in marine
 RT sponges";
 RL J. Cell. Sci. 112:4305-4313(1999).
 DR EMBL; Y18438; CAC38779.1; -
 DR HSSP; P30041; IPRX.
 DR GO; GO:0004601; F:peroxidase activity; IEA.
 DR InterPro; IPR000866; AhpC-TSA.
 DR Pfam; PF00578; AhpC-TSA; 1.
 KW Peroxidase.
 SQ SEQUENCE 217 AA; 24131 MW; 924PAC1550F63B0B CRC64;
 Query Match 52.4%; Score 625.5; DB 2; Length 217;
 Best Local Similarity 52.3%; Pred. No. 1.7e-50;
 Matches 116; Conservative 38; Mismatches 63; Indels 5; Gaps 4;
 QY 1 MELNLGDSPPDQAEALGAEHRLHYLGDSWGMFSPNDPTVCTTELAEAVKLQDSF 60
 Db 1 MP-LNQQIFPNFEADTTGEP-IKFHDWLGDMGILFSPHPRDTPVCTTELTGTVAKLVPEF 58
 QY 61 TKKNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPFLVCDPNRELAASLGIMDPAEKD 120
 Db 59 QRKNVVKVIAISCDPVDSHKTIWKIDIESY-GKLUSSFGYPIIADKNRELAQVFGMLDPDEKD 117
 QY 121 KKGKPLTCRCVFFISPEKKLAASILYPATTGGRNFABILRVLDLSQLTAKFPVATPVDMTA 180
 Db 118 KAGLPLTARAVFIIGDPKKLSLLYPATTGGRNFDEILRVDSQLTAYKKVATPANWKN 177
 QY 181 GAKCCVVPNLAAEAQRLLPKGHEALQLPSGKPYRLTDPDR 222
 Db 178 GKCMILPSVSKDEAKF--PGVETADVPSSGKKYIRLADQPK 217
 RESULT 16
 Q6P624
 ID Q6P624 PRELIMINARY; PRT; 224 AA.
 AC Q6P624;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein MGC76137.
 GN Names=MGC76137;
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8364;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahney J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	
RA	Krzywinski M.I., Stalska U., Smallos D.E., Schnerch A., Schein J.E.,	
RA	Jones S.J., Marra M.A.;	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Embryo;	
RL	Klein S., Gerhard D.S.;	
RL	Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC062510; AAH62510.1; ..	
DR	Hypothetical protein.	
QY	SEQUENCE 224 AA; 25156 MW; 5C4813E444AF7AB CRC64;	
QY	Query Match 52.0%; Score 621; DB 2; Length 224;	
QY	Best Local Similarity 54.0%; Pred. No. 4.8e-50;	
QY	Matches 122; Conservative 33; Mismatches 65; Indels 6; Gaps 4;	
Qy	1 MP-LNLGDSFPDFAE-ALGAEHPRLEHYLGDSGWMPFSDHNDFTPVCTTELAEAVKLQD 58	
Db	1 MPGLLGEIFPDFAETTTIG--RIKHEFLGSGWLVFSDHPRDTPVCTTELGRVCVKLAP 58	
Qy	59 SFTKKNCKLVGFSNDLQSHREWAKDIMAY--AGRSGNLPPLVCDPNRELAASIGIMDP 116	
Db	59 EFKRNVRMTALSIDSVDHGLGWSNCSNCDSTETLPPFIADPKRDVAVKLGMJDP 118	
Qy	117 AEKDKGGLPTCRCVFFRISPEPKLAASILYPATTGRNFAETLRVLDSLQLTAKFPVATPV 176	
Db	119 DEKDMQGPVTARCFFIIGPKMKLSILYPATTGRNFEILRVVDSLQLTAVHNATPV 178	
Qy	177 DWTAGAKCCVVPNLAABEAQRLPKGHEALQLPSGKPYLRITPPDR 222	
Db	179 DWKPGDRVVPVNPVPEBAASKLPSGVFNKALPSRKNLYRVTAPQ 224	
RESULT 17		
Q7SYQ4	PRELIMINARY; PRT; 224 AA.	
AC	Q7SYQ4;	
DT	01-OCT-2003 (TrEMBLrel. 25, Created)	
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)	
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
DE	MG664582 protein.	
GN	Name=MG664582;	
OS	Xenopus laevis (African clawed frog).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;	
OC	Xenopodinae; Xenopus.	
OX	NCBI_TaxID=8355;	
RP	[1]	
RN	SEQUENCE FROM N.A.	
RC	TISSUE=Whole;	
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA	Datchenko L., Marziani K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,	
RA	Brownstein M.J., Udén T.B., Toshiki S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,	
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahney J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	

[illegible]

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Qy 3 LNLGDSFPDFOAALGAHFLRHLHYLGDSWGMFMSHPNDFTPVCTTTELAAVQLQDSFTK 62
Db 2 VNLGDVPFNFTANTSKGE- IKFHDWLGSMALLFSHPADYTPVCTTTELARVVTLLAPEFEK 60
Qy 63 KNYKLVGFCNDLQSHREAWKDIWAYA-GRSGNLPFLPLVCDPNRELAASIGIMDPAEKDK 121
Db 61 RGVKLIALSCDGVNSHVGMGVDNVTFFAGQKDDLPYPIVADDEERKLAELGMDIDPDBERTK 120
Qy 122 KGLPLTCRCVFFISPEKKLAASILYLPATTGRNFAEILRLVDSLSQLTAKFPVATPDVDTAG 181
Db 121 EGLPLTARAVFIIGDKKLKLSLYLPATTGRNFNGILRVDSLSQLTATQKVATPDVWEKG 180
Qy 182 AKCCVVPNLAAEAAQRLLPKGHEALQPLSGKPYLRLLTP 219
Db 181 QKCMVLPITPMDEARKLFP-NMEVRDVPESGEGYLRFPT 217

RESULT 19
Q95WZ7
ID Q95WZ7 PRELIMINARY; PRT; 221 AA.
AC Q95WZ7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glutathione peroxidase.
GN Name=gph;
OS Ixodes scapularis (Black-legged tick) (Deer tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Ixodes.
OX NCBI_TaxID=6945;
RN [1]
RP SEQUENCE FROM N.A.
RA Das S., Banerjee G., DePonte K., Marcantonio N., Kantor F.S.,
RA Fikrig E.;
RT "Salp5D, an Ixodes scapularis antioxidant, is one of 14
RT immunomodulant antigens in engorged tick salivary glands.";
RL J. Infect. Dis. 184:0-0(2001).
DR EMBL; AF209911; AAK97814.1; -.
DR HSP; P30041; 1PRX.
DR GO; GO:0004601; F:peroxidase activity; IEA.
DR InterPro; IPR000866; AhpC-TSA.
DR Pfam; PF00578; AhpC-TSA; 1.
KW Peroxidase.
SQ SEQUENCE 221 AA; 24566 MW; AB287CD3F3B34B50 CRC64;

Query Match 51.8%; Score 619; DB 2; Length 221;
Best Local Similarity 51.8%; Pred. No. 7.3e-50;
Matches 114; Conservative 35; Mismatches 69; Indels 2; Gaps 2;

Qy 2 PLNLGDSFPDFOAALGAHFLRHLHYLGDSWGMFMSHPNDFTPVCTTTELAAVQLQDSFT 61
Db 3 PLNLGDSFPNFTCDTTEGK-IDFHEWLGNSWGLFSLFPADYTPVCTSELARAAQLHHVQ 61
Qy 62 KKNKLVGFCNDLQSHREAWKDIWAYA-GRSGNLPFLPLVCDPNRELAASIGIMDPAEKDK 120
Db 62 KKGKVLIALSCDVSVEHSGRMKIDINAFGELPDGPFYPIADEKRDIAVKLGMLDPVEKD 121
Qy 121 KKGKLVTCRCVFFISPEKKLAASILYLPATTGRNFAEILRLVDSLSQLTAKFPVATPDVDTA 180
Db 122 KEGPLTLCRAVFIIGDKKLKLSLYLPATTGRNFNGILRVDSLSQLTATQKVATPDVWEKG 181
Qy 181 GAKCCVVPNLAAEAAQRLLPKGHEALQPLSGKPYLRLLTPD 220
Db 182 GTPCMVLPSTVEEILKLFPTGIKQYEVPSGKNYLRITMD 221

RESULT 20
Q9USAI
ID Q9USAI PRELIMINARY; PRT; 235 AA.
AC Q9USAI;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Thioethoxin peroxidase.
OS Dirofilaria immitis (Canine heartworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Dirofilaria.
OX NCBI_TaxID=6287;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20189524; PubMed=10726990;
RA Chandrashekar R., Tsuji N., Morales T.H., Carmody A.B., Ozols V.O.,
RA Walton J., Tang L.;
RT "Removal of hydrogen peroxide by a l-cysteine peroxidoxin enzyme of
RT the filarial parasite Dirofilaria immitis.";
RL Parasitol. Res. 86:200-206(2000).
DR EMBL; AF045164; AAF21097.1; -.
DR HSP; P30041; 1PRX.
DR GO; GO:0004601; F:peroxidase activity; IEA.
DR InterPro; IPR000866; AhpC-TSA.
DR Pfam; PF00578; AhpC-TSA; 1.
KW Peroxidase.
SQ SEQUENCE 235 AA; 26298 MW; D177468FA6B47576 CRC64;

Query Match 51.8%; Score 618.5; DB 2; Length 235;
Best Local Similarity 54.1%; Pred. No. 8.8e-50;
Matches 124; Conservative 28; Mismatches 66; Indels 11; Gaps 3;

Qy 5 LGDSFPDFOAALGAHFLRHLHYLG-DSWGMFMSHPNDFTPVCTTTELAAVQLQDSFTKK 63
Db 7 LGDRFPDFRAETNEGFIPIFYDWIGKDSMAILFSHPDRDFTPVCTTTELARVLQLAPEPKR 66
Qy 64 NCKLVGFCNDLQSHREAWKDIWAYA-GRSGNLPFLPLVCDPNRELAASIGI 113
Db 67 NVKLIGLSCDSAESHRKWDVDDINAVCKMKCNDGDTCCSGNKLFPPIADENRFLATELGM 126
Qy 114 MDAPEKDKKGLPLTCRCVFFISPEKKLAASILYLPATTGRNFAEILRLVDSLSQLTAKFPV 173
Db 127 MDPDERDENGALTCRVFIIGPEKTLKLSILYLPATTGRNFAEILRLVDSLSQLTAVKLA 186
Qy 174 TPVDWTAGAKCCVVPNLAAEAAQRLLPKGHEALQPLSGKPYLRLLTPDP 222
Db 187 TPVDWKGDDCVLPTIDTTEAKKLGKEINTIEFSGKHYLRWVAHPK 235

RESULT 21
1CPX DIRIM
ID 1CPX DIRIM STANDARD; PRT; 235 AA.
AC 017433;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 1-Cys peroxidoxin (EC 1.11.1.7) (1-CysPxn).
OS Dirofilaria immitis (Canine heartworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Dirofilaria.
OX NCBI_TaxID=6287;
RN [1]
RP SEQUENCE FROM N.A.
RA McGonigle S., James E.R.;
RA "1-Cys peroxidoxin from Dirofilaria immitis.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Thiol specific antioxidant.
CC -1- CATALYTIC ACTIVITY: Donor + H(2)O(2) = oxidized donor + 2 H(2)O.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- PTM: Cys-49 is the site of oxidation by H(2)O(2). The oxidized
CC intermediate might be Cys-SOH (By similarity).
CC -1- SIMILARITY: Belongs to the ahpC/TSA family. Redoxin subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/

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RA Hayaehida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Oheato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN
RP
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayaehida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Oheato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; AK029613; BAC26531.1; -;
DR ENBL; AK077012; BAC36564.1; -;
DR HSSP; P30041; 1PRX.
DR MGD; MGI:133688; Prdx6-rel.
DR InterPro; IPR000866; Ahpc-TSA.
DR Pfam; PF00578; Ahpc-TSA; 1.
SQ SEQUENCE 224 AA; 24996 MW; CC30B869EA99026 CRC64;

Query Match 50.9%; Score 607.5; DB 2; Length 224;
Best Local Similarity 52.7%; Pred. No. 8.9e-49;
Matches 119; Conservative 32; Mismatches 68; Indels 7; Gaps 4;

QY 1 MP--LNLGDSFPDFQAE-ALGAHFRHLHEYLGDWGMVFSHPNDFTPVCTTLEAAVKLQ 57
DB 1 MPGGLLIGEAPDFEANTTIG--RIRPHDFLNSGWMFLFSHPKDFTPVCTTELGRAAKLA 58

QY 58 DSTTKNCKLVGSCNDLQSHREWAKDIMAYAGRS--GNLPFLVCDPNRELAASLGIMD 115
DB 59 PEFKRNKVLIALSVDSVEHLAWSKDINAYGATPKPEKLFPFIIDDKDRDISILFCMLD 118

QY 116 PAEKDKKGLPLTCRCVFFISPEKLAASILYPATTGNFNAEILRLVDSLQLTAKFPVATP 175
DB 119 PVKEDANSMLTARGVIFIGFDKKLKMSLYPSNSTGRNFEILRLVDSLQLTETKPVATP 178

QY 176 VDWTAGKCCVVPNLAEEAQRLLPKGHEALQPLSGKPYLRLTPDP 221
DB 179 VDMKKGESVMVLPDLPEEAACRFPFGKISTTKLPKSGKNLYRYTPQ 224

RESULT 24
Q694A9
ID Q694A9 PRELIMINARY; PRT; 222 AA.
AC Q694A9
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative peroxiredoxin.
OS Glossina morsitans morsitans.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Hippoboscidae; Glossinidae; Glossina.
OX NCBI_TaxID=37546;
RN
RP
RC SEQUENCE FROM N.A.
RA Munks R.J.L., Grail W., Igglesden T.J., Lehane M.J.:
RT "Antioxidant genes from the Tsetse fly Glossina morsitans morsitans."
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR ENBL; AY625503; AAT85820.1; -;

DR InterPro; IPR000866; Ahpc-TSA.
DR Pfam; PF00578; Ahpc-TSA; 1.
SQ SEQUENCE 222 AA; 25002 MW; 0A228CC383CB4526 CRC64;

Query Match 50.2%; Score 599; DB 2; Length 222;
Best Local Similarity 49.5%; Pred. No. 5.5e-48;
Matches 110; Conservative 38; Mismatches 66; Indels 8; Gaps 3;

QY 3 LNLGDSFPDFQAEALGAHFRHLHEYLGDWGMVFSHPNDFTPVCTTLEAAVKLQDSFTK 62
DB 6 LNLGDSFPDFQAEALGAHFRHLHEYLGDWGMVFSHPNDFTPVCTTLEAAVKLQDSFTK 64

QY 63 KNCVLGVGSCNDLQSHREWAKDIMAYAGRSNLP---FPLVCDPNRELAASLGIMDPAEK 119
DB 65 RNKPIALSCTVETHTKGMIEDIKSY---GKLPXVDYPIIGDKERKLAVKLNLMDKDEI 120

QY 120 DKGLPLTCRCVFFISPEKLAASILYPATTGNFNAEILRLVDSLQLTAKFPVATPVDWT 179
DB 121 NAEGLPMTCAVFIQVDSKGLRLQILYPATTGNFNAEILRLVDSLQLTAKFPVATPVDWT 180

QY 180 AGAKCCVVPNLAEEAQRLLPKGHEALQPLSGKPYLRLTPDP 221
DB 181 QGETCMILPTVSDXASRKYPKGFKTINVPSPKPYMRQTPQ 222

RESULT 25
TSA ONCVO
ID TSA ONCVO STANDARD; PRT; 232 AA.
AC P52570;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Thiol-specific antioxidant.
GN Name-TSA;
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN
RP SEQUENCE FROM N.A.
RA Chandrasekar R., Curtis K.C., Weil G.J.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 62-222 FROM N.A.
RA Chandrasekar R., Curtis K., Weil G.J.;
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ahpc/TSA family. Remydrin subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U31052; AAC27392.1; -;
CC EMBL; U09385; AAS50214.2; -;
CC HSSP; P30041; 1PRX.
CC InterPro; IPR000866; Ahpc-TSA.
CC Pfam; PF00578; Ahpc-TSA; 1.
CC Antioxidant.
FT ACT SITE 49 49 By similarity.
SQ SEQUENCE 232 AA; 25925 MW; 029E93F276232B37 CRC64;

Query Match 50.2%; Score 599; DB 1; Length 232;
Best Local Similarity 51.5%; Pred. No. 5.9e-48;
Matches 118; Conservative 30; Mismatches 73; Indels 8; Gaps 2;

QY 2 PLNLGDSFPDFQAEALGAHFRHLHEYLGDWGMVFSHPNDFTPVCTTLEAAVKLQDSF 60
DB 4 PPSGPNKFPDFQAEALGAHFRHLHEYLGDWGMVFSHPNDFTPVCTTLEAAVKLQDSF 63

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QY 61 TKKNCKLVGFCNDLQSHREWAKDIMAY-----AGRSNLPFPPLVCDPNRELAASLGI 113
DB 64 KKRNVKLIJGLSCDSADSHSKWADILALYRMKCVGCDSEKKLPFYPIIADDESLATELGM 123
QY 114 MPAEKDKKGLPLTRCVCFFISPEKLAASILYPATTGRNFAELRLVDSLOLTAKFPVA 173
DB 124 MPEDEDEKGNLTARCVIIGSDKTLKLSILYPATTGRNFAELRLVDSLOLTAVKVA 183
QY 174 TPVDMTAGKCCVVPNLAEEAQRLLPKGHEALQPSGKPYRLTDPDR 222
DB 184 TPVDMKGDGCVLPTIDNEAKKLFGEKHTITIDPSGKHLYLRMVHPK 232

RESULT 26
Q7QIQ4 PRELIMINARY; PRT; 249 AA.
AC Q7QIQ4; (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DE AGCP3392 (Fragment)
GN Name=agCG54406; ORFNames=ENSGANG00000012627;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008807; EAA04146.1; -.
DR InterPro; IPR000866; AhpC-TSA.
DR Pfam; PF00578; AhpC-TSA; 1.
FT NON_TER 1
SQ SEQUENCE 249 AA; 27277 MW; 8D3591162B8832DE CRC64;

Query Match 49.9%; Score 595.5; DB 2; Length 249;
Best Local Similarity 52.7%; Pred. No. 1.4e-47;
Matches 118; Conservative 28; Mismatches 73; Indels 5; Gaps 3;

QY 1 MPLNLGDSFPDFOAE-ALGAEHRLHEYLGDSGVMFSPNDFTPVCTTELAEAVKLQDS 59
DB 27 MSLNLGDPFPNFTADTTIGDIFD--HQWIGDGWAILFSPADYTPVCTTELAAVAKLVE 84
QY 60 FTKKNCKLVGFCNDLQSHREWAKDIMAY--AGRSNLPFPPLVCDPNRELAASLGI 117
DB 85 FTKRNVKPTALSCTVESHGRGWIEDIKAYGQLAAADPPFPPIIDDSKRELAVKLNMLDRD 144
QY 118 EKDKKGLPLTRCVCFFISPEKLAASILYPATTGRNFAELRLVDSLOLTAKFPVATPVD 177
DB 145 EIGSAGLPLTRCRAVVIDACKKRLSLILYPATTGRNFAELRLVIDSLQITDKRVATPAD 204
QY 178 WTAGAKCCVVPNLAEEAQRLLPKGHEALQPSGKPYRLTDPDP 221
DB 205 WMPGDSQWQPTVPADQLATLPAGVDSVTLPSGKQYLKRTCEP 248

RESULT 27
Q9GPQ2 PRELIMINARY; PRT; 222 AA.
AC Q9GPQ2; (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DE 1-cys peroxiredoxin Dfx-6005.
GN Name=Prx6005;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

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OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=21534478; PubMed=11677042; DOI=10.1016/S0891-5849(01)00692-X;
RA Radvuk S.N., Klitchko V.I., Spinola B., Sohal R.S., Orr W.C.;
RT "The peroxiredoxin gene family in Drosophila melanogaster.";
RL Free Radic. Biol. Med. 31:1090-1100(2001).
DR EMBL; AF3111878; AAG47822.1; -.
DR HSP; P30041; 1PRX.
DR FLYBase; FBgn0031479; Prx6005.
DR InterPro; IPR000866; AhpC-TSA.
DR Pfam; PF00578; AhpC-TSA; 1.
SQ SEQUENCE 222 AA; 24841 MW; 6FBA23BEBDA66318 CRC64;

Query Match 49.2%; Score 588; DB 2; Length 222;
Best Local Similarity 49.3%; Pred. No. 6e-47;
Matches 108; Conservative 38; Mismatches 71; Indels 2; Gaps 2;

QY 3 LNLGDSFPDFOAEALGAEHRLHEYLGDSGVMFSPNDFTPVCTTELAEAVKLQDSFTK 62
DB 6 LNLGDSFPNFTAE-SEGRIIDFYDMQDSWAILFSPADYTPVCTTELSRAALIPFEQK 64
QY 63 KNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPFPPLVCDPNRELAASLGI 122
DB 65 RVGKPIALSCDPVESHKGWIEDIKSF-GKLSGDFYPIIADDESLATELGM 123
QY 123 GLPLTRCVCFFISPEKLAASILYPATTGRNFAELRLVDSLOLTAKFPVATPVDWDTAG 182
DB 124 GIPLTRCRAVVIDACKKRLSLILYPATTGRNFAELRLVIDSLQITQKSVATPADWKQGG 183
QY 183 KCVVPNLAEEAQRLLPKGHEALQPSGKPYRLTDPDP 221
DB 184 KCVLPFTVKAEDVPKFLPDGDIETIELPSGKSYLRITPQP 222

RESULT 28
Q9VQI7 PRELIMINARY; PRT; 222 AA.
AC Q9VQI7; (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE CG3083-PA.
GN Name=Prx6005; ORFNames=CG3083;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutcliffe G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Aghayani A., An H.J., Andrews-Pfannkuch C., Baldwin D.,
RA Balles R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

```


OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
OX NCBI TaxID=3880;

[1] — SEQUENCE FROM N.A.
 RN Boudet J., Buitink J., Satour P., Leprince O.H.L.;
 RA Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AY594329; AAT67997.1; -
 DR InterPro: IPR000866; AbpC-TSA.
 DR Pfam: PF00578; AbpC-TSA; 1.
 DR SO SEQUENCE 218 AA; 24414 MW; B5C138B69F698CE4 CRC64;

Query Match	42.6%	Score 509;	DB 2;	Length 218;
Best Local Similarity	42.5%	Pred. NO. 1.5e-39;		
Matches 93;	Conservative 44;	Mismatches 78;	Indels 4;	Gaps 4;

Qy 1 MP-LNLGDSFPDQAEALGAEHFRLHEYLGDSCWGMFSPHNDFTPVCTTTELAERAVKLQDS 59

Db 1 MPGLTIGTIPDLLEVDVDTTQK-K-ILKLHPCSDSWTILFHPGDDFTPVCTTTELGKMAQYASE 59

Qy	60	FTKQVKLVGFSNDLQSHREWAKDIMAYAGRSNGLPPPLVCDPNRELAAASLGIMDPAEK	119
	:	:	:
Dd	60	FNRGRVMLLGMSCDLSEHKWTKDIEART-PCGAKVNPYIIISPKPREIKQLNVNDDPEK	118
	:	:	:

Qy	120	DKKGLPLTCRCVPFISPEKKLAASILYPATTTGRNFAEILRVLSQLTAKFPVATPVDMT	179
D5	119	DSNG-NLPSRALHIVGPKKKLSFLYPAQTGRNMDEVLRVLSQKASKYKIATPANWK	177

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Qy      180 AGAKCCVVVNLAEEAQRLLPKGHEALQLPSGKPYRLT 218
Db      178 PGPEVWISPDVTNDQAEFMFPGQFKTADLPSEKKEYLRPT 216

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RESULT 37
REHY ORYSA

ID	REHY_ORYSA	STANDARD;	PRT;	220 AA.
AC	P52573;			
DT	01-OCT-1996	(Rel. 34, Created)		
DT	01-OCT-1996	(Rel. 34, Last sequence update)		

DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RAB24 protein.
OS Oryza sativa (Rice).
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Erihartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
EN 11

RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica / Yuhkara;
RA Fujino K., Tanaka K., Xu Z., Kikuta Y.;
R1 submitted, (oct-1995), cv. b. pmbr/cv. pmt/nnar database

CC	-I- INDUCTION: By abscisic acid (ABA).
CC	-I- SIMILARITY: Belongs to the abcC/tSA family. Rehydrin subfamily.
CC	THIS GENE PROMOTED TO ORIGINALLY BE CONVERTED TO A GENE THAT IS EXPRESSED THROUGHOUT CELL DEVELOPMENT.

CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC altered.⁵³

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DR PIR; T03967; T03967.
DR HSP; P30041, 1PRX.
DR Gramene; P52573; c.

DR	Pfam:	PF00578; AhpC-TSA; 1.
KW	Antioxidant.	46
FT	ACT-Site	46

By similarity.

Query Match	42.6†	Score	508.5	DB 1	Length	220
Best Local Similarity	43.6†	Pred. No.	1.7e-39			

Matches 96; Conservative 46; Mismatches 73; Indels 5; Gaps 4;

Qy	MP-1	MP-2	MP-3	MP-4	MP-5	MP-6	MP-7	MP-8	MP-9	MP-10	MP-11	MP-12	MP-13	MP-14	MP-15	MP-16	MP-17	MP-18	MP-19	MP-20	MP-21	MP-22	MP-23	MP-24	MP-25	MP-26	MP-27	MP-28	MP-29	MP-30	MP-31	MP-32	MP-33	MP-34	MP-35	MP-36	MP-37	MP-38	MP-39	MP-40	MP-41	MP-42	MP-43	MP-44	MP-45	MP-46	MP-47	MP-48	MP-49	MP-50	MP-51	MP-52	MP-53	MP-54	MP-55	MP-56	MP-57	MP-58	MP-59	MP-60	MP-61	MP-62	MP-63	MP-64	MP-65	MP-66	MP-67	MP-68	MP-69	MP-70	MP-71	MP-72	MP-73	MP-74	MP-75	MP-76	MP-77	MP-78	MP-79	MP-80	MP-81	MP-82	MP-83	MP-84	MP-85	MP-86	MP-87	MP-88	MP-89	MP-90	MP-91	MP-92	MP-93	MP-94	MP-95	MP-96	MP-97	MP-98	MP-99	MP-100	MP-101	MP-102	MP-103	MP-104	MP-105	MP-106	MP-107	MP-108	MP-109	MP-110	MP-111	MP-112	MP-113	MP-114	MP-115	MP-116	MP-117	MP-118	MP-119	MP-120	MP-121	MP-122	MP-123	MP-124	MP-125	MP-126	MP-127	MP-128	MP-129	MP-130	MP-131	MP-132	MP-133	MP-134	MP-135	MP-136	MP-137	MP-138	MP-139	MP-140	MP-141	MP-142	MP-143	MP-144	MP-145	MP-146	MP-147	MP-148	MP-149	MP-150	MP-151	MP-152	MP-153	MP-154	MP-155	MP-156	MP-157	MP-158	MP-159	MP-160	MP-161	MP-162	MP-163	MP-164	MP-165	MP-166	MP-167	MP-168	MP-169	MP-170	MP-171	MP-172	MP-173	MP-174	MP-175	MP-176	MP-177	MP-178	MP-179	MP-180	MP-181	MP-182	MP-183	MP-184	MP-185	MP-186	MP-187	MP-188	MP-189	MP-190	MP-191	MP-192	MP-193	MP-194	MP-195	MP-196	MP-197	MP-198	MP-199	MP-200	MP-201	MP-202	MP-203	MP-204	MP-205	MP-206	MP-207	MP-208	MP-209	MP-210	MP-211	MP-212	MP-213	MP-214	MP-215	MP-216	MP-217	MP-218	MP-219	MP-220	MP-221	MP-222	MP-223	MP-224	MP-225	MP-226	MP-227	MP-228	MP-229	MP-230	MP-231	MP-232	MP-233	MP-234	MP-235	MP-236	MP-237	MP-238	MP-239	MP-240	MP-241	MP-242	MP-243	MP-244	MP-245	MP-246	MP-247	MP-248	MP-249	MP-250	MP-251	MP-252	MP-253	MP-254	MP-255	MP-256	MP-257	MP-258	MP-259	MP-260	MP-261	MP-262	MP-263	MP-264	MP-265	MP-266	MP-267	MP-268	MP-269	MP-270	MP-271	MP-272	MP-273	MP-274	MP-275	MP-276	MP-277	MP-278	MP-279	MP-280	MP-281	MP-282	MP-283	MP-284	MP-285	MP-286	MP-287	MP-288	MP-289	MP-290	MP-291	MP-292	MP-293	MP-294	MP-295	MP-296	MP-297	MP-298	MP-299	MP-300	MP-301	MP-302	MP-303	MP-304	MP-305	MP-306	MP-307	MP-308	MP-309	MP-310	MP-311	MP-312	MP-313	MP-314	MP-315	MP-316	MP-317	MP-318	MP-319	MP-320	MP-321	MP-322	MP-323	MP-324	MP-325	MP-326	MP-327	MP-328	MP-329	MP-330	MP-331	MP-332	MP-333	MP-334	MP-335	MP-336	MP-337	MP-338	MP-339	MP-340	MP-341	MP-342	MP-343	MP-344	MP-345	MP-346	MP-347	MP-348	MP-349	MP-350	MP-351	MP-352	MP-353	MP-354	MP-355	MP-356	MP-357	MP-358	MP-359	MP-360	MP-361	MP-362	MP-363	MP-364	MP-365	MP-366	MP-367	MP-368	MP-369	MP-370	MP-371	MP-372	MP-373	MP-374	MP-375	MP-376	MP-377	MP-378	MP-379	MP-380	MP-
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Qy	60	FTKKNCKLVCFSCNDLOSHREWAKDIMAYAGRSN--LPFLVCDPNRELAASLGIMDPAE	118
Db	60	FDKRGVKLGISCDVQSHKDFKDI EAY--KPGNRVTYPIMADPGREAIKOLNMVDPDE	117

Qy	119	KDKKGLPLTCRCVFPISPEKKLAASILYPATTGRNPAEILRLVDSLQLTAKFPVATPVDW	178
Db	118	KDSNGGHLPSRALHTVGPDKVKLSFLYPACVGRNNDEVVRAVDAQLTAARTLRLATPNW	177

Qy	179	TAGAKCCVVPNLAEEAQRLLPKGHEALQLPSGKPYLRLT	218
		: : : : : :	
		: : : : : :	
Db	178	KPGEDFVIPGVSDDEAKEFPQGFDTDADLPSSGKGYLRF	217
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RESULT 38
Q8DGG4

ID				PRI;	ZII AA.
Q8DQ4				PRELIMINARY;	
AC					
Q8DQ4;					
DT	(TReMBLrel. 23,			Created)	
DT	01-MAR-2003				
DT	(TReMBLrel. 23,			Last sequence update)	
DT	01-MAR-2003				

01-JUN-2003 (iREMBLrel. 24, Last annotation update)
DE AtpC/TSA family protein.
DT OrderedLocusNames=tlr2261;
OS Sneathococcus elongatus
GN Sneathococcus elongatus (Thermosynechococcus elongatus).
QN

OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
[1] _____
RP SEQUENCE FROM N.A.
RP

RC STRAIN=BP-1;
RX MEDLINE=22225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
PA waranabe A., Iriguchi M. Kawasaki K. Kimura T. Kishida Y.

RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimojo S., Sugimoto M., Matsumoto M., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
RT *Thermosynechococcus elongatus* BP-1".
PT *Thermosynechococcus elongatus* BP-1".

RL DNA Res. 9:123-130(2002).
 DR EMBL; AP005376; BAC09813.1; -.
 DR HSP: P30041; 1PRX.
 DR IPI: ipr000856. AbTC-TSA

DR	Pfam; PF00578; AhpC-TSA; 1.
KW	Complete proteome.
SQ	SEQUENCE 211 AA; 23861 MW; 6FB5E8913545A16F CRC64;

Query Match 42.1%; Score 503; DB 2; Length 211;
Best Local Similarity 45.5%; pred. No. 5.4e-39;
Matches 101; Conservative 44; Mismatches 53; Indels 14; Gaps 5;

Qy	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
db	1	MSL	KL	GD	VV	VN	FT	Q	AS	M	G	N	I	N	F	--	Y	E	W	A	G	S	W	V	L	F	S	H	P	A	D	T	P	V	C	T	T	E	L	E	A	A	V	K	L	Q	S	D	59																																																			
Qy	1	M	P	L	N	L	G	D	S	F	P	D	F	--	Q	A	E	A	G	A	E	H	R	L	H	E	I	L	G	D	S	G	W	G	V	M	F	S	H	P	N	D	F	T	P	V	C	T	T	E	L	E	A	A	V	K	L	Q	S	D	58																																							

Qy	60	FTKKNCKLVGFS	CNDLQSHREWAK	DI MAYAGRS	GNLFPFLV	CDPNRRELAAS	LGIMDPAEK	119
Db	59	PEKRNKKVALSV	DSESHLGWIKL	EEV--NNVK	VDYPI	LADKKVSTY	YDMIHNSL	116

[illegible]

Qy	180	AGAKCCVYNLAEEERQLLPKGHEALQLPSGKPYLRLLTPDP	221
		: : : :	
Db	173	EGQEIVVPVSUSDEAKPKPGFNAV-----KPYRLRLLTPQ	209

RESULT 39
Q694A7

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AC Q994A7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Putative peroxiredoxin.
OS Glossina morsitans morsitans.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Hippoboscidae; Glossinidae; Glossina.
OX NCBI_TaxID=37546;
RN [1]
RP SEQUENCE FROM N.A.
RA Munks R.J.L., Grail W., Igglesden T.J., Lehan M.J.;
RT "Antioxidant genes from the Tsetse fly Glossina morsitans morsitans.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY625505; AAT85822.1; -.
DR InterPro; IPR000866; AhpC-TSA.
DR Pfam; PF00578; AhpC-TSA; 1.
DR NCBI_TaxID=37546;
SQ SEQUENCE 220 AA; 24796 MW; C76E0744F3760477 CRC64;

Query Match 42.1%; Score 502.5; DB 2; Length 220;
Best Local Similarity 45.0%; Pred. No. 6.3e-39;
Matches 98; Conservative 39; Mismatches 78; Indels 3; Gaps 3;

QY 3 LNLGDSFPDQAEALGAHFLRHEYLGLDWSGVMFSPHNDFTPVCTTTELAEAVKLQDSFTK 62
DB 1 MRLNSVVPDFKADSTKGP-IQFYDWQGSWVLLFSPHSDFTPVCTTTELGRIAVNAGQFAK 59
QY 63 KNCKLVGFCNDLQSHREWAKDIMAY-AGRSGNLPPPLVCDPNRELAASLGIMDPAEKDK 121
DB 60 RNTKCLAHSDVDDTQSHINWYNDIKSYCADIRGEFFPFPILADPNRQLAISLGMIDEXQRDD 119
QY 122 KGLPLTCRCVFFTSPEKKLAASILYPATTGRTNFAEILRVLDLSLQLTAKF-PVATPVDWTA 180
DB 120 PESAKTVRALFISPDHVRSLMFPYPTTGRNVDEILRCIDSLSLQLTDRFKAVATPANWMP 179
QY 181 GAKCCVVPNLAAEEAQRLLPKGHEALQLPSGKPYLRLT 218
DB 180 GSKVMILPSITDEAAKLFPGFDRTSMPSGGNYVRTT 217

RESULT 40
Q9GFPQ1 PRELIMINARY; PRT; 220 AA.
AC Q9GFPQ1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 1-cys peroxiredoxin DPX-2540-1.
GN Name=Prx2540-2; Synonyms=Prx2540-1;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21534478; PubMed=11677042; DOI=10.1016/S0891-5849(01)00692-X;
RA Radvuk S.N., Klichko V.I., Spinola B., Sohal R.S., Orr W.C.;
RT "The peroxiredoxin gene family in Drosophila melanogaster.";
RL Free Radic. Biol. Med. 31:1090-1100(2001).
DR EMBL; AF3111879; AAG47823.1; -.
DR HSP; P30041; IPRX.
DR FlyBase; FBgn0033520; Prx2540-1.
DR FlyBase; FBgn0033518; Prx2540-2.
DR InterPro; IPR000866; AhpC-TSA.
DR Pfam; PF00578; AhpC-TSA; 1.
DR NCBI_TaxID=7227;
SQ SEQUENCE 220 AA; 24770 MW; 85AA0223EF7BFE38 CRC64;

Query Match 42.0%; Score 501.5; DB 2; Length 220;
Best Local Similarity 44.5%; Pred. No. 7.9e-39;
Matches 97; Conservative 39; Mismatches 79; Indels 3; Gaps 3;
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QY 3 LNLGDSFPDQAEALGAHFLRHEYLGLDWSGVMFSPHNDFTPVCTTTELAEAVKLQDSFTK 62
DB 1 MRLNSVVPDFKADSTKGP-IQFYDWQGSWVLLFSPHSDFTPVCTTTELGRIAVNAGQFAK 59
QY 63 KNCKLVGFCNDLQSHREWAKDIMAY-AGRSGNLPPPLVCDPNRELAASLGIMDPAEKDK 121
DB 60 RNTKCLAHSDVDDTQSHINWYNDIKSYCADIRGEFFPFPILADPNRQLAISLGMIDEXQRDD 119
QY 122 KGLPLTCRCVFFTSPEKKLAASILYPATTGRTNFAEILRVLDLSLQLTAKF-PVATPVDWTA 180
DB 120 PESAKTVRALFISPDHVRSLMFPYPTTGRNVDEILRCIDSLSLQLTDRFKAVATPANWMP 179
QY 181 GAKCCVVPNLAAEEAQRLLPKGHEALQLPSGKPYLRLT 218
DB 180 GSKVMILPSITDEAAKLFPGFDRTSMPSGGNYVRTT 217
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Search completed: October 28, 2005, 21:50:00
Job time : 182 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2005, 21:35:13 ; Search time 40 Seconds
(without alignments)
536.408 Million cell updates/sec

Title: US-10-723-123-3

Perfect score: 1194

Sequence: 1 MPLNLGDSFPDFOAALGAE.....EALQLPSGKPYLRLTPDPRG 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	508.5	42.6	220	2 T03967	RAB24 protein - ri
2	497.5	41.7	212	2 G83215	probable antioxidant
3	495	41.5	218	2 S60285	B15C protein - bar
4	492	41.2	211	2 S77532	rehydrin - Syncho
5	478	40.0	202	2 S22499	hypothetical prote
6	458.5	38.4	212	2 AD2356	AhpC/TSA family pr
7	437	36.5	243	2 T18224	rehydrin protein h
8	420	35.2	261	2 S39825	hypothetical prote
9	403	33.8	218	2 AH2758	conserved hypothet
10	403	33.8	218	2 E97539	rehydrin (imported
11	400	33.5	219	2 A95978	probable anti-oxid
12	330.5	27.7	222	2 E70374	alkyl hydroperoxid
13	290.5	24.3	195	2 F69283	alkyl hydroperoxid
14	285.5	23.9	222	2 H64391	alkyl hydroperoxid
15	283.5	23.7	215	2 H72330	hypothetical prote
16	271	22.7	215	2 S74033	alkyl hydroperoxid
17	262	21.9	226	2 B69079	alkyl hydroperoxid
18	261.5	21.9	216	2 C71065	probable alkyl hyd
19	258.5	21.6	209	2 S51098	probable peroxid
20	258.5	21.6	216	2 C75081	probable peroxid
21	248.5	20.8	250	2 B72454	probable thioresox
22	240	20.1	242	2 S49173	hypothetical prote
23	235.5	19.7	210	2 T06318	thiol-specific ant
24	225.5	18.9	265	2 T09211	bas1 protein - spi
25	220	18.4	181	2 AD1638	2-cys peroxidexoi
26	219	18.3	197	2 C84951	alkyl hydroperoxid
27	218	18.3	181	2 AD1275	2-cys peroxidexoi
28	215	18.0	195	2 A43858	alkyl hydroperoxid
29	213	17.8	195	2 S71013	alkyl hydroperoxid

30	E13	17.8	195	2 B70679	alkyl hydroperoxid
31	209	17.5	180	2 B69867	2-cys peroxidexoi
32	205.5	17.2	178	2 S29119	hypothetical prote
33	204.5	17.1	183	2 A83983	2-cys peroxidexoi
34	203	17.0	203	2 A12385	peroxidexoin (imp
35	202.5	17.0	226	2 S43598	mers homolog R07E5
36	202	16.9	200	2 S76284	hypothetical prote
37	199.5	16.7	195	2 E87164	alkyl hydroperoxid
38	197.5	16.5	195	2 G71492	probable thio-spec
39	195.5	16.4	198	2 C64715	alkyl hydroperoxid
40	195	16.3	200	2 I51016	proliferation asso
41	193.5	16.2	188	2 D71314	probable alkyl hyd
42	193	16.2	196	2 H86587	thio-specific anti
43	193	16.2	196	2 E72036	thio-specific anti
44	191.5	16.0	198	2 H71801	probable peroxidase
45	191	16.0	199	2 A48513	macrophage 23K str

ALIGNMENTS

RESULT 1

T03967

RAB24 protein - rice

C:Species: Oryza sativa (rice)

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C:Accession: T03967; PC4271

R:Fujino, K.; Tanaka, K.; Xu, Z.; Kikuta, Y.

submitted to the EMBL Data Library, August 1997

A:Description: ABA-responsive 24kDa polypeptide from rice calli is related to the thiol

A:Reference number: Z15166

A:Accession: T03967

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-220 <FUJ>

A:Cross-references: UNIPROT:P52573; EMBL:D63917; PIDN:BAA09947.1

A:Experimental source: cv. Yuhkara

R:Kawakami, T.; Kamo, M.; Chen, M.C.; Taugita, A.

submitted to JIPID, April 1997

A:Reference number: PC4267

A:Accession: PC4271

A:Molecule type: protein

A:Residues: 2-15 <KAW>

C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 pro

Query Match 42.6%; Score 508.5; DB 2; Length 220;

Best Local Similarity 43.6%; Pred. No. 1.6e-38;

Matches 96; Conservative 46; Mismatches 73; Indels 5; Gaps 4;

QY 1 MP-LNLGDSFPDFOAALGAEHRLHEYLGDSDGVMFSPHNDFTPVCTTLEAAVKLQDS 59

DB 1 MPGLTIGDTVPNLELSTHGK-IRIHDFVGDTVILFSPHGDFTPVCTTLEAAMAAYAKE 59

QY 60 FTKNCKLVGFCNDLQSHREAWKIDIMAYAGRSNGN-LPPFLVCDPNRELAASIGIMDPAE 118

DB 60 FDRKGVKLLGISCDVQSHKDFKDI EAY--KPGNRVTYPI MADPSREAIKQLMMVDPDE 117

QY 119 KDKKGLPLTCRCVFFISPEKLAASILYPATTCGNFAEILRVLDLSLQLTAKFPVATVDW 178

DB 118 KDSNGGHLPSRALHIVGPKVKLSFLYPACVGRNMDVVRAVDALQTAARLATPVNW 177

QY 179 TAGAKCWWPNLAAEAQRLLPKGHEALQLPSGKPYLRLT 218

DB 178 KPGEFPVPPGVSDDEAKEKFPQGFDTADLPSCGYLRFT 217

RESULT 2

G83215

probable antioxidant protein PA3450 [imported] - Pseudomonas aeruginosa (strain PAO1)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C:Accession: G83215

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; E

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G83215
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-212 <STO>
A;Cross-references: UNIPROT:Q9HYF6; GB:AB004765; GB:AB004091; NID:g9949580; PIDN:AAG0683
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA3450
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 protein

Query Match 41.7%; Score 497.5; DB 2; Length 212;
Best Local Similarity 46.8%; Pred. No. 1.5e-37;
Matches 104; Conservative 34; Mismatches 71; Indels 13; Gaps 5;

QY 1 MFLNLGDSFPDFAEALGAHFLRHLHEYLGDGSGVMFSPHNDFTPVCTTTELAEAVKLQDSF 60
Db 1 MSRLGDIAPDFEQDS-SEGRIRLHEWLGDGSGVLFSPHDPFTPVCTTTELGTAKLKQDF 59

QY 61 TKKNCKLVGFSNCDLQSHREWAKDIMAYAGSGNLPFLVCDPNRELAASLGIMDPAEK 120
Db 60 AQGVKVLALUSDVPVESHKWKIIDDINETQDTRVN--FPFIADADRKVSELDYDIHNAND 117

QY 121 KKGGLPLTCRCVFFISPEKKLAASILYPATTGRNFABEILRVLDLSQLTAKFPVATPVDTWA 180
Db 118 ---TLTVRSFLFIIDPSKKVRLIITYPASTGRNFNEILRVLDLSQLTDEHKVATPANWED 173

QY 181 GAKCCVVPNLA-ABEAQRLLPKGHEALQLPSGKPYLRLTPDP 221
Db 174 GDEWIVPSLKDDEEIKRRFPKGYRAV-----KPYLRLTPQ 210

RESULT 3
S60285
B5C protein - barley
C;Species: Hordeum vulgare (barley)
C;Date: 20-Jul-1996 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: S60285
R;Aalen, R.B.; Opsahl-Ferstad, H.G.; Linnestad, C.; Olsen, O.A.
Plant J. 5, 385-396, 1994
A;Title: Transcripts encoding an oleosin and a dormancy-related protein are present in barley
A;Reference number: S60284; MUID:94236153; PMID:8180622
A;Accession: S60285
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-218 <AAL>
A;Cross-references: UNIPROT:P52572; EMBL:X76605; NID:g471320; PIDN:CAA54066.1; PID:g4713
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 protein

Query Match 41.5%; Score 495; DB 2; Length 218;
Best Local Similarity 43.4%; Pred. No. 2.7e-37;
Matches 95; Conservative 43; Mismatches 77; Indels 4; Gaps 4;

QY 1 MP-LNLGDSFPDFAEALGAHFLRHLHEYLGDGSGVMFSPHNDFTPVCTTTELAEAVKLQDS 59
Db 1 MPGLTIGDTPVNLDELSTHGK-IRIHDYVGVGVILFSPHGDFTPVCTTTELAAMANYAKE 59

QY 60 FTKKNCKLVGFSNCDLQSHREWAKDIMAYAGSGNLPFLVCDPNRELAASLGIMDPAEK 119
Db 60 FEKRGVLLGLISCDVDVQSHKEWTNIDIEAYKPGS-KVTYPIIMADPDRSAIKQLNNVDPDEK 118

QY 120 DKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFABEILRVLDLSQLTAKFPVATPVDTW 179
Db 119 DAQG-QLPSTLHVIGPKVKVLSFLYPSCTGRNMDVVRVAVDSLLTAAGHKVATPANWK 177

QY 180 AGAKCCVVPNLAABEAQRLLPKGHEALQLPSGKPYLRLT 218
Db 178 PGECWVIAPGVDSBEAKMFPQGFETADLPSSKGYLRF 216

RESULT 4

S77532

rehydriin - *Synechocystis* sp. (strain PCC 6803)

N;Alternate names: protein slr1198

C;Species: *Synechocystis* sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C;Accession: S77532

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.

O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud

DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*

s.

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S77532

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-211 <KAN>

A;Cross-references: UNIPROT:P73348; EMBL:D90905; GB:AB001339; NID:g1652360; PIDN:BAAL173

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 protein

Qy 143 SILYPATTGRNFABILRVLDLSQLTAKFPVATPVDMWTAGAKCCVVPNLAABEAQRLLPKG 202
Db 125 SFLYPSCTGRNMDVWRAVDSLLTAAXKHVATPANWKPGEVCWTPAGVDSBEAKKLPQG 184
Qy 203 HEALQLPSGKPYRLT 218
Db 185 FETKDLPSKGYLRFT 200

RESULT 6
AD2356
AhpC/TSA family protein [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AD2356
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Saamoto, S.; Watanabe, A.; Iriuguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AD2356
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-212 <KUR>
A:Cross-references: UNIPROT:Q8YP05; GB:BA000019; PIDN:BAB76103.1; PID:g17133540; GSPDB:G
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr4404
C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 prot

Query Match 38.4%; Score 458.5; DB 2; Length 212;
Best Local Similarity 44.4%; Pred. No. 5.1e-34;
Matches 99; Conservative 33; Mismatches 76; Indels 15; Gaps 6;
Qy 1 MPLNLGSPDPF-QAELGAEHRLHEYLGDWSGVMSHPNDFTPVCTTELAELAVKLQDS 59
Db 1 MALRLGDTVPNFTQASTHGDIDF--YAWAGDSWVLFSPADYTPVCTTELGTVAKLKPE 58
Qy 60 FTKKNCCKLVGSCNDLQSHREWAKDIMAYAGRSNGLPPLVCDPNRELAASLGIMDPAEK 119
Db 59 FDKRNVKAIASLVDDVESHNGWGDII--ETQSTLTNLPILADNRKVSOLDYMIHPI-- 113
Qy 120 DKGLPLTCRCVFFISPEKKLAASILYPATTGRNFABILRVLDLSQLTAKFPVATPVDMWT 179
Db 114 -NANAATVRSVFIDENKKLRLFTTYPSTGRNFDELLRVLDLSQLTQDNYSVATPADWK 172
Qy 180 AGAKCCVVPNLAABEA-QRLLPKGHEALQLPSGKPYRLTDPDP 221
Db 173 DGDKWVIVPSLKDPVLKELKFPKGYEVV-----KPYLRLTQPQ 210

RESULT 7
T18224
rehydrin protein homolog - yeast (Candida albicans)
C:Species: Candida albicans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18224
R:Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, November 1998
A:Reference number: Z18831
A:Accession: T18224
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-243 <BAR>
A:Cross-references: UNIPROT:O94014; EMBL:AL033396; PIDN:CAA21951.1
C:Genetics:
A:Note: Ca35A5.08
C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 prot

Query Match 36.6%; Score 437; DB 2; Length 243;
Best Local Similarity 41.4%; Pred. No. 5.3e-32;
Matches 91; Conservative 41; Mismatches 76; Indels 12; Gaps 5;

Qy 3 LNLGDSPPDQABALGAEHRLHEYLGDWSGVMSHPNDFTPVCTTELAELAVKLQDSFTK 62
Db 27 LRLGSTAPDFKADTTNGP-ISPFEHYIGDSWAILFSPHAARTSVCTSELSAFARLEPEFTK 85
Qy 63 KNCCKLVGFSNCLQSHREWAKDIMAYAGRSNGLPPLVCDPNRELAASLGIMDPAEK--- 119
Db 86 RGVKLLAISADPVEANSWDIMDEDFSG--SRVKFPIIADAERKAVATLYDMIDHQDATNL 143
Qy 120 DKGLPLTCRCVFFISPEKKLAASILYPATTGRNFABILRVLDLSQLTAKFPVATPVDMWT 179
Db 144 DDGKLQTLIRAVFIIDPSKKIRLIMITYPASTGRNTAEVLRVLDLSQLVDKQKVITPINWV 203
Qy 180 AGAKCCVVPNLAABEAQRLLPKGHEALQLPSGKPYRLTLP 219
Db 204 PGDDVLVHMGVPDDEARVLPFK-YRAI-----KPYIRLTLP 237

RESULT 8
S39825
hypothetical protein YBL064c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein YBL0503; hypothetical protein YBL0524
C:Species: Saccharomyces cerevisiae
C:Date: 16-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C:Accession: S39825; S45799; S37326
R:Scherens, B.; el Bakkoury, M.; Vierendeels, F.; Dubois, E.; Messenguy, F.
Yeast 9, 1355-1371, 1993
A:Title: Sequencing and functional analysis of a 32 560 bp segment on the left arm of y
A:Reference number: S39824; MUID:94205266; PMID:8154187
A:Accession: S39825
A:Molecule type: DNA
A:Residues: 1-261 <SCH>
A:Cross-references: UNIPROT:P34227; EMBL:Z23261; NID:g313733; PIDN:CAA80784.1; PID:g313
A:Experimental source: strain S288C
R:Dubois, E.; El Bakkoury, M.; Glansdorff, N.; Messenguy, F.; Pierard, A.; Scherens, B
submitted to the Protein Sequence Database, August 1994
A:Reference number: S45782
A:Accession: S45799
A:Molecule type: DNA
A:Residues: 1-261 <DUB>
A:Cross-references: EMBL:Z35825; NID:g536100; PIDN:CAA84884.1; PID:g536101; MIPS:YBL064
A:Experimental source: strain S288C
C:Genetics:
A:Map position: 2L
C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 pro
F;S2-188/Domain: alkyl hydroperoxidase c22 protein homology <C22>

Query Match 35.2%; Score 420; DB 2; Length 261;
Best Local Similarity 41.8%; Pred. No. 2e-30;
Matches 92; Conservative 41; Mismatches 73; Indels 14; Gaps 6;
Qy 3 LNLGDSPPDQAB-ALGAEHRLHEYLGDWSGVMSHPNDFTPVCTTELAELAVKLQDSFT 61
Db 49 LRINSDAPNFDADTTVTKINF--YDYLGDWSGVLFSPHADFTPVCTTEVSFAKLKPEFD 106
Qy 62 KNCCKLVGFSNCLQSHREWAKDIMAYAGRSNGLPPLVCDPNRELAASLGIMDPAEKDK 121
Db 107 KRNKVLIGLSVEDVESHEKWIQIKEIA-KRVNKGPIIGDTFRNVAFLVDMVD-ABGFK 164
Qy 122 K---GLPLTCRCVFFISPEKKLAASILYPATTGRNFABILRVLDLSQLTAKFPVATPVDM 178
Db 165 NINDGSLKTVRSVFVIDPKKIRLIFTYPSTVGRNTSEVLRLVDALQLTDKEGVVTTINW 224
Qy 179 TAGAKCCVVPNLAABEAQRLLPKGHEALQLPSGKPYRLLT 218
Db 225 QPADDDVIIPSPVSNDEAKAKFGQFNEI-----KPYLRFT 258

RESULT 9
AH2758
conserved hypothetical protein Atul480 [imported] - Agrobacterium tumefaciens (strain C
C:Species: Agrobacterium tumefaciens

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AH2758
R;Wood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gilet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
star, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AH2758
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-218 <KUR>
A;Cross-references: UNIPROT:Q8UFBB; GB:AE008688; PIDN:AAL42486.1; PID:g17739903; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atul480
A;Map position: circular chromosome
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 pro
Query Match 33.8%; Score 403; DB 2; Length 218;
Best Local Similarity 39.4%; Pred. No. 5.5e-29;
Matches 89; Conservative 31; Mismatches 92; Indels 14; Gaps 4;
QY 1 MPLNLGDSPPDFOAALGAHFLHLEHYLGDSWGMFNSHPNDFTPVCTTTELAEAVKLQDSF 60
Db 1 MSRLINDIAPDFTAETTQGP-VRFPHDWIGDGMWVLFSPKNTFTPVCTTELGA MGGLQPEF 59
QY 61 TKNCKLVGSCNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELA-----ASLGIMD 115
Db 60 EKRGVKIIGISVDPVESHKWKADIRATG--FNVDYPLIGDKDLKVAKYDMLPAGAGD 117
QY 116 PAEKDKKGLPLTCRCVFFTSPEKKLAASILYPATTGRNFAEILRLVDSLQLTAKFPVATP 175
Db 118 SSGRTPADNATVRSVFVIGPDKKIKLVLTYPMTTGRNFDLRAIDSLQLTAKHQVATP 177
QY 176 VDMTAGKCCVVPNLAAEBAORLLPKGHEALQLPSPKPYRLRTPDP 221
Db 178 ANWKGEDVIITAAVSNEDAIARFGSYDTVL-----PYLRKTKQP 217
RESULT 10
E97539
renydrin [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: E97539
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourullo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: E97539
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-218 <KUR>
A;Cross-references: UNIPROT:Q8UFBB; GB:AE007869; PIDN:AAK87270.1; PID:g15156560; GSPDB:G
C;Genetics:
A;Gene: AGR C 2729
A;Map position: circular chromosome
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 pro
Query Match 33.8%; Score 403; DB 2; Length 218;
Best Local Similarity 39.4%; Pred. No. 5.5e-29;
Matches 89; Conservative 31; Mismatches 92; Indels 14; Gaps 4;
QY 1 MPLNLGDSPPDFOAALGAHFLHLEHYLGDSWGMFNSHPNDFTPVCTTTELAEAVKLQDSF 60
Db 1 MSRLINDIAPDFTAETTQGP-VRFPHDWIGDGMWVLFSPKNTFTPVCTTELGA MGGLQPEF 59
QY 61 TKNCKLVGSCNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELA-----ASLGIMD 115

Db 60 EKRGVKIIGISVDPVESHKWKADIRATG--FNVDYPLIGDKDLKVAKYDMLPAGAGD 117
QY 116 PAEKDKKGLPLTCRCVFFTSPEKKLAASILYPATTGRNFAEILRLVDSLQLTAKFPVATP 175
Db 118 SSGRTPADNATVRSVFVIGPDKKIKLVLTYPMTTGRNFDLRAIDSLQLTAKHQVATP 177
QY 176 VDMTAGKCCVVPNLAAEBAORLLPKGHEALQLPSPKPYRLRTPDP 221
Db 178 ANWKGEDVIITAAVSNEDAIARFGSYDTVL-----PYLRKTKQP 217
RESULT 11
A95978
probable anti-oxidant protein, AhpCTS family [imported] - Sinorhizobium meliloti (stra
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: A95978
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Herna
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing end
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: A95978
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-219 <KUR>
A;Cross-references: UNIPROT:Q9R9R2; GB:AL591985; PIDN:CAC49489.1; PID:g15140976; GSPDB:G
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
pela, D.; Chain, P.; Cowie, A.; Davies, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
hebaul, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Welle, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: Smb20964
A;Genome: plasmid
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 pro
Query Match 33.5%; Score 400; DB 2; Length 219;
Best Local Similarity 40.6%; Pred. No. 1e-28;
Matches 93; Conservative 33; Mismatches 83; Indels 20; Gaps 8;
QY 1 MPLNLGDSPPDFOAAL-GAEHFLHLEHYLGDSWGMFNSHPNDFTPVCTTTELAEAVKLQDS 59
Db 1 MSRLINDIAPDFTAETTQGTINF--HEMIGDGMWVLFSPKNTFTPVCTTELGA MGAGIEPE 58
QY 60 FTKNCKLVGSCNDLQSHREWAKDIMAYAGRSNLPPLVCDPNREL-AASLGIMDPA- 117
Db 59 FRKRGVKIIGISVDPVESHKWKNDIKVATG--FEVDYPLIGD--RDLKVAKYDMLPAG 114
QY 118 --EKDKKGLP---LTCRCVFFTSPEKKLAASILYPATTGRNFAEILRLVDSLQLTAKFPV 172
Db 115 AGTSEGRTPADNATVRSVFVIGPDKKIKLVLTYPMTTGRNFEILRAIDSLQLTAKHQV 174
QY 173 ATPVDWTAGAKCCVVPNLAAEBAORLLPKGHEALQLPSPKPYRLRTPDP 221
Db 175 ATPANWQGEDVIITAAVSNEDAVQRFGSFDTVL-----PYLRKTKQP 217
RESULT 12
E70374
alkyl hydroperoxide reductase - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: E70374
R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320

QY 61 TKKNCKLVGSCNDLQSHREWAKDIMAYAGRSNLPFPPLVCDPNRELAASLGIMDPAEKD 120
Db 63 RKLNTLGLISDQVFSHIKWIEMKLG--VEIEFPVIADDLGVSRRLLIHP-----116
QY 121 KKGPLTCTRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPVDTA 180
Db 117 NKGTN-TVRAVFVDNGIIRALVYYPQEVGRNIDILRAVKALQTSDEKGAIPANWPS 175
QY 181 GA----KCCVVPNLAEEAQRLL 199
Db 176 NELINDSVIIPPASSVEEARKRL 198
RESULT 16
S74033
alkyl hydroperoxide reductase homolog - Sulfolobus solfataricus
N;Alternate names: protein c0215
C;Species: Sulfolobus solfataricus
C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: S74033
R;Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S.
Mol. Microbiol. 22, 175-191, 1996
A;Title: Organizational characteristics and information content of an archaeal genome: 1
A;Reference number: S73076; MUID:97055432; PMID:8899719
A;Accession: S74033
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-215 <SEN>
A;Cross-references: UNIPROT:P95895; EMBL:Y08256; NID:g1707679; PIDN:CAA69447.1; PID:g170
A;Experimental source: strain P2
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996
C;Superfamily: alkyl hydroperoxide reductase c22 protein; alkyl hydroperoxidase c22 pro
Query Match 22.7%; Score 271; DB 2; Length 215;
Best Local Similarity 31.4%; Pred. No. 4.6e-17;
Matches 69; Conservative 35; Mismatches 88; Indels 28; Gaps 7;
QY 1 MPLNLGDSFPFOAEALGAEHFRLHYLGDSWGMFSPHNDFTPVCTTTELAEAVKLQDSF 60
Db 6 IPL-IGERPPEMEVITTOGRILKLPDDYKG-RWVLFSPHGDFTPVCTTFYSFAKKYEEF 63
QY 61 TKKNCKLVGSCNDLQSHREWAKDIMAYAGRSNLPFPPLVCDPNRELAASLGIMD 116
Db 64 KKLNTLGLISVDSNISHIEMWIEKNLV-----EIPFPIADPMGNVAKRLGMI--115
QY 117 AEKDKKGLPLTCTRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPV 176
Db 116 ---HAQSSTATVRAVFVDDKGVRLIILYYPMEIGNIDEILRAIRALQLVDRAGVVTPA 172
QY 177 DWTAGAKCCVVPN--LAABEAQRLLPKGHEALQLPSGKPY 214
Db 173 NW-----PNNELIGDKVINPAPRTIKDAKRWLGQPF 203
RESULT 17
B69079
alkyl hydroperoxide reductase - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 11-Jun-1999
C;Accession: B69079
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiawani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
A;Reference number: A6900; MUID:98037514; PMID:9371463
A;Accession: B69079
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-226 <MTH>
A;Cross-references: GB:AE000804; GB:AE000666; NID:g2621196; PIDN:AAB84665.1; PID:g262120
A;Experimental source: strain Delta H

C;Genetics:
A;Gene: MTH159
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 pro
Query Match 21.9%; Score 262; DB 2; Length 226;
Best Local Similarity 33.7%; Pred. No. 3.2e-16;
Matches 60; Conservative 33; Mismatches 75; Indels 10; Gaps 5;
QY 1 MPLNLGDSFPFOAEALGAEHFRLHYLGDSWGMFSPHNDFTPVCTTTELAEAVKLQDSF 60
Db 18 MPL-IGDKPPEMEVQTGPMELPDDEFEG-KWFIILFSPHADFTPVCTTFEFAVQEVPEL 75
QY 61 TKKNCKLVGSCNDLQSHREWAKDIMAYAGRSNLPFPPLVCDPNRELAASLGIMDPAEKD 120
Db 76 RELDCELVGLSDQVFSHIKWIEMIA--ENLDETEFFVIADTGR-VADTLGLIHPARPT 132
QY 121 KKGPLTCTRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPV 178
Db 133 N-----TVRAVFVDPEGIIRAILYYPQELGRNIEIVRMIRAFRVIDAEGVAAPANW 185
RESULT 18
C71065
probable alkyl hydroperoxide reductase - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 16-Aug-2004
C;Accession: C71065
R;Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: C71065
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-216 <KAW>
A;Cross-references: UNIPROT:O58966; GB:AP000005; NID:g3236132; PIDN:BAA30317.1; PID:g32
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH1217
Query Match 21.9%; Score 261.5; DB 2; Length 216;
Best Local Similarity 32.4%; Pred. No. 3.3e-16;
Matches 66; Conservative 36; Mismatches 77; Indels 25; Gaps 7;
QY 5 LGDSFPFOAEALGAEH--FRLHEYL--GDSWGMFSPHNDFTPVCTTTELAEAVKLQDSF 60
Db 4 IGEKPEVEVK---TTHGVIKLPDYFTKQGWFIILFSPHADFTPVCTTFEYGMQKRVVEF 60
QY 61 TKKNCKLVGSCNDLQSH--REWAKDIMAYAGRSNLPFPPLVCDPNRELAASLGIMDPA 117
Db 61 RKLGVPEIGLSVDQVFSHIKWIEMKDNL-----SVEIDFPVIADDRGELAEKLGMI---112
QY 118 EKDKKGLPLTCTRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPV 177
Db 113 ----PSGATITAKRAVFVDDKGIIRALVYYPQEVGRNIDILRVKALKISTEKGVALPHK 169
QY 178 W-----TAGAKCCVVPNLAEEAQR 197
Db 170 WPNNELIGDKVINPAPASTIEKKQ 193
RESULT 19
S51098
probable alkyl hydroperoxide reductase (EC 1.6.4.-) - Methanobacterium thermoautotroph
N;Alternate names: hypothetical protein k
C;Species: Methanobacterium thermoautotrophicum
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S51098
R;Meile, L.; Fischer, K.; Jenal, U.; Leisinger, T.
submitted to the EMBL Data Library, July 1993
A;Description: Molecular characterization of a superoxide dismutase gene from Methanoba

N;Alternate names: Avi-3 antigen
C;Species: Mycobacterium avium
C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A43858; T09655
R;Yamaguchi, R.; Matsuo, K.; Yamazaki, A.; Takahashi, M.; Fukasawa, Y.; Wada, M.; Abe, Y.;
Infect. Immun. 60, 1210-1216, 1992
A;Title: Cloning and expression of the gene for the Avi-3 antigen of Mycobacterium avium
A;Reference number: A43858; MUID:92175967; PMID:1371765
A;Accession: A43858
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-195 <YAM>
A;Cross-references: UNIPROT:Q57413; GB:U18263; NID:g1040852; PIDN:AAA79917.1; PID:g8411
A;Note: sequence extracted from NCBI backbone (NCBIN:85445, NCBIP:85446)
R;Sherman, D.R.; Sabo, P.J.; Hickey, M.J.; Arain, T.M.; Mahairas, G.G.; Yuan, Y.; Barry
Proc. Natl. Acad. Sci. U.S.A. 92, 6625-6629, 1995
A;Title: Disparate responses to oxidative stress in saprophytic and pathogenic mycobact
A;Reference number: Z16801; MUID:95327698; PMID:7604044
A;Accession: T09655
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-195 <SHE>
A;Cross-references: EMBL:U18263; NID:g1040852; PIDN:AAA79917.1; PID:g841168
C;Genetics:
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 pro
F;23-162/Domain: alkyl hydroperoxidase c22 protein homology <C22>

Query Match 18.0%; Score 215; DB 2; Length 195;
Best Local Similarity 31.0%; Pred. No. 4.7e-12;
Matches 57; Conservative 32; Mismatches 61; Indels 34; Gaps 7;

Qy 1 MP-LNLGDSPPDFOAEALGA-----EHPRL---HEYLGDSGWMFSPNDPTP 44
Db 1 MPLLTTGDDQPPAYELTALTAGDLSKVDAKQPGDYFTTITSEDHAG-KWRVVFVFPKDTF 59
Qy 45 VCTTELAEAVKLQDSFTKKNCKLVGFSNCLQSHREWA---KDIMAYAGRSNLPFPLVC 101
Db 60 VCPTETATFGKLNDEFEDRDRAQVLGVISDFVHFVFNWRAQHDLK-----NLPFFMLS 112
Qy 102 DPNRELAASLGIMDPAEKKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFABILRLV 161
Db 113 DIKRELSLATGVLNAD-----GVADRATFIVDPNNEIQFVSVTAGSVGRNVEEVLRLV 165
Qy 162 DSLQ 165
Db 166 DALQ 169

RESULT 29
S71013
alkyl hydroperoxide reductase chain C - Mycobacterium bovis
C;Species: Mycobacterium bovis
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
C;Accession: S71013; S71011
R;Wilson, T.M.; Collins, D.M.
Mol. Microbiol. 19, 1025-1034, 1996
A;Title: ahpc, A gene involved in isoniazid resistance of the Mycobacterium tuberculosis
A;Reference number: S71011; MUID:96249696; PMID:8830260
A;Accession: S71013
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-195 <WIL>
A;Cross-references: UNIPROT:Q57348; EMBL:U24083; NID:g1002370; PIDN:AAB60203.1; PID:g10
A;Experimental source: ATCC 35723
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
A;Accession: S71011
A;Molecule type: DNA
A;Residues: 1-195 <WIL>
A;Cross-references: EMBL:U24084; NID:g1002373; PIDN:AAB38112.1; PID:g1002374
A;Experimental source: ATCC 35729
C;Genetics:

A;Molecule type: DNA
A;Residues: 1-197 <STO>
A;Cross-references: GB:AP000398; GSPDB:GNO0144
C;Experimental source: strain APS
C;Genetics:
A;Gene: ahpc; BU182
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 prot

Query Match 18.3%; Score 219; DB 2; Length 197;
Best Local Similarity 30.5%; Pred. No. 2.1e-12;
Matches 54; Conservative 29; Mismatches 82; Indels 12; Gaps 3;

Qy 10 PDFQAEAL-----GAEHLRLHEYLGDGWMFSPNDPTPVCVTTTELAEAVKLQDSFTKKN 64
Db 9 PNFTAPAILKNNQIVEQFDLKKYNGQSTVLFFWPMDFTFVCPSEIIIEFNKLHSEFKRN 68
Qy 65 CKLVGFSNCLQSHREWAKDIMAYAGRSNLPFPLVCDPNRELAASLGIMDPAEKDKKGL 124
Db 69 VKIVGVSDISVYVHOAW-QNTLPKNGGIGKINFFPMVSDVXHDIIQKSYGIQHP-----NL 121
Qy 125 PLTCRCVFFISPEKKLAASILYPATTGRNFABILRLVLSLQLTAKFPVATPVDMWTAG 181
Db 122 GIALRASFLDSNWIIIRHQVNDLPFGRTYDMIRWVDALDFHNKFGVEVCPANWKG 178

RESULT 27
AD1275
2-cys peroxidoxin homolog lmol604 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD1275
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Faihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitounam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vasquez-Boland, J.A.; Vosse, H.; Wehlend,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1275
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-181 <GLA>
A;Cross-references: UNIPROT:Q8Y6S9; GB:NC_003210; PIDN:CAC99682.1; PID:g16411033; GSPDB:
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmol604
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 prot

Query Match 18.3%; Score 218; DB 2; Length 181;
Best Local Similarity 28.9%; Pred. No. 2.3e-12;
Matches 54; Conservative 37; Mismatches 80; Indels 16; Gaps 6;

Qy 5 LGDSFPDFOAEALGAEH-----FRLHEYL-GDSGWMFSPNDPTPVCVTTTELAEAVKLQDS 59
Db 6 VGTQAPRFEMAEAVNPNTFGKVSLKNIEDDKWTLFFYPMDFTFVCPTEIVAISARSD 65
Qy 60 FTKKNCKLVGFSNCLQSHREWAKDIMAYAGRSNLPFPLVCDPNRELAASLGIMDPAEK 119
Db 66 FDALNARIIGASTDTHSHLAWNTPTPIKEGG-IGKLNYPAAADTNHQVASYDGLV----I 120
Qy 120 DKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFABILRLVLSLQLTAKFPVATPVDMT 179
Db 121 EEEGVAL--RGLFLINPKGIQIEVHHNIGREVEVLRLVQLQQTGG-----LCPINWQ 174
Qy 180 AGAKCCV 186
Db 175 PGKTIIV 181

RESULT 28
A43858
alkyl hydroperoxidase C (EC 1.6.4.-) - Mycobacterium avium

N;Alternate names: Avi-3 antigen
C;Species: Mycobacterium avium
C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A43858; T09655
R;Yamaguchi, R.; Matsuo, K.; Yamazaki, A.; Takahashi, M.; Fukasawa, Y.; Wada, M.; Abe, Y.;
Infect. Immun. 60, 1210-1216, 1992
A;Title: Cloning and expression of the gene for the Avi-3 antigen of Mycobacterium avium
A;Reference number: A43858; MUID:92175967; PMID:1371765
A;Accession: A43858
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-195 <YAM>
A;Cross-references: UNIPROT:Q57413; GB:U18263; NID:g1040852; PIDN:AAA79917.1; PID:g8411
A;Note: sequence extracted from NCBI backbone (NCBIN:85445, NCBIP:85446)
R;Sherman, D.R.; Sabo, P.J.; Hickey, M.J.; Arain, T.M.; Mahairas, G.G.; Yuan, Y.; Barry
Proc. Natl. Acad. Sci. U.S.A. 92, 6625-6629, 1995
A;Title: Disparate responses to oxidative stress in saprophytic and pathogenic mycobact
A;Reference number: Z16801; MUID:95327698; PMID:7604044
A;Accession: T09655
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-195 <SHE>
A;Cross-references: EMBL:U18263; NID:g1040852; PIDN:AAA79917.1; PID:g841168
C;Genetics:
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 pro
F;23-162/Domain: alkyl hydroperoxidase c22 protein homology <C22>

Query Match 18.0%; Score 215; DB 2; Length 195;
Best Local Similarity 31.0%; Pred. No. 4.7e-12;
Matches 57; Conservative 32; Mismatches 61; Indels 34; Gaps 7;

Qy 1 MP-LNLGDSPPDFOAEALGA-----EHPRL---HEYLGDSGWMFSPNDPTP 44
Db 1 MPLLTTGDDQPPAYELTALTAGDLSKVDAKQPGDYFTTITSEDHAG-KWRVVFVFPKDTF 59
Qy 45 VCTTELAEAVKLQDSFTKKNCKLVGFSNCLQSHREWA---KDIMAYAGRSNLPFPLVC 101
Db 60 VCPTETATFGKLNDEFEDRDRAQVLGVISDFVHFVFNWRAQHDLK-----NLPFFMLS 112
Qy 102 DPNRELAASLGIMDPAEKKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFABILRLV 161
Db 113 DIKRELSLATGVLNAD-----GVADRATFIVDPNNEIQFVSVTAGSVGRNVEEVLRLV 165
Qy 162 DSLQ 165
Db 166 DALQ 169

RESULT 29
S71013
alkyl hydroperoxide reductase chain C - Mycobacterium bovis
C;Species: Mycobacterium bovis
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
C;Accession: S71013; S71011
R;Wilson, T.M.; Collins, D.M.
Mol. Microbiol. 19, 1025-1034, 1996
A;Title: ahpc, A gene involved in isoniazid resistance of the Mycobacterium tuberculosis
A;Reference number: S71011; MUID:96249696; PMID:8830260
A;Accession: S71013
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-195 <WIL>
A;Cross-references: UNIPROT:Q57348; EMBL:U24083; NID:g1002370; PIDN:AAB60203.1; PID:g10
A;Experimental source: ATCC 35723
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
A;Accession: S71011
A;Molecule type: DNA
A;Residues: 1-195 <WIL>
A;Cross-references: EMBL:U24084; NID:g1002373; PIDN:AAB38112.1; PID:g1002374
A;Experimental source: ATCC 35729
C;Genetics:

	Matches	57;	Conservative	31;	Mismatches	76;	Indels	19;	Gaps	7;
Qy	5	LGDSFPDFQAEAL-----GAEHFRLHYLGDSWGVMFSHPNDFTPVCTTTELAAEAVKLQDS	59							
Dd	5	VGKPAPEFMKAVKGDRGGFTFEVKLDGYKG-KWLVMFFYPLDFTFVCPTTEITGFSKRAEE	63							
Qy	60	FTKNCKNLGVSCNDLQSHREWA-KDTWAGARGSNLPFLPLVCDPNRELAAISIGIMDPAE	118							
Dd	64	FRDLKAELLAVSCDSQSSETWTINODIK--QGGLGKINFPIASDKTTVEVSTKYGI-----Q	117							
Qy	119	KDKKGLPLTCRCVFIFISPEKKLAASIILYPATTGNFAEILRVLDSLTQLTAKEPVPATVDW	178							
Dd	118	IEEGISU--RGLFIIDPEGIVRYSVVHDLNVGRKSVDETLRVLKAFOTGG----MCALDW	171							
Qy	179	TAG 181								
Dd	172	HEG 174								
 RESULT 33										
A	A83983									
C	2-cys peroxiredoxin BH2665 [imported] - Bacillus halodurans (strain C-125)									
C	Species: Bacillus halodurans									
C	Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004									
C	Accession: A83983									
R	Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai									
Nucleic Acids Res.	28, 4317-4331, 2000									
A	Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and									
A	Reference number: A83650; MUID:20512582; PMID:11058132									
A	Accession: A83983									
A	Status: preliminary									
A	Molecule type: DNA									
A	Residues: 1-183 <STO>									
A	Cross-references: UNIPROT:Q9K9I2; GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB063									
A	Experimental source: strain C-125									
A	Genetics:									
A	Gene: BH2665									
C	Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 prot									
Query Match	17.1%; Score 204.5; DB 2; Length 183;									
Best Local Similarity	32.2%; Pred No. 3.9e-11;									
Matches	49; Conservative 26; Mismatches 64; Indels 11; Gaps 4;									
Qy	30	DSWGVMFSHPNDFTPVCTTTELAAEAVKLQDSFTTKNKCLGVGFSCNDLQSHREWAKDIMAYA	89							
Dd	37	DKMTLVFFYPMDFTFVCPTTEITSLSRDYDEFEDLDAEVICGSTDTTHHKAWINTSRDDN	96							
Qy	90	GRSNNLPPLVCDPNRELAAISLMGMDPAEKDGKGLPLTCRCVFIFISPEKKLAASIIYPAT	149							
Dd	97	G-LGDLKPYLAADTNHVSREYGVL---JEEEGIAL--RGLFIISPEGELMYSVVNHN	149							
Qy	150	TGRNFASILRVLDSLQLTAKEPVPATVDWTAG 181								
Dd	150	IGRDVDETLLRVLQAQTGG----LC PANWKPG 177								
 RESULT 34										
A	AI2385									
C	peroxiredoxin [imported] - Nostoc sp. (strain PCC 7120)									
C	Species: Nostoc sp. PCC 7120									
A	Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120									
C	Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004									
C	Accession: AI2385									
R	Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi									
Nakazaki, N.; Shimpo, S.										
DNA Res.	8, 205-213, 2001									
A	Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana									
A	Reference number: AB1807; MUID:21595285; PMID:11759840									
A	Accession: AI2385									
A	Status: preliminary									
A	Molecule type: DNA									
A	Residues: 1-203 <KUR>									
A	Cross-references: UNIPROT:Q8YNC5; GB:BA0000019; PIDN:BAB76340.1; PID:g17133778; GSPDB:B									

R; Kaneo, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.
O, K.; Okumura, S.; Shimpou, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996

A; Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*

s.

A; Reference number: S74322; MUID: 97061201; PMID: 8905231

A; Accession: S76284

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-200 <KAN>

A; Cross-references: UNIPROT-Q55624; EMBL-D64000; GB-AB001339; NID-gl001484; PIDN:BAA1013

A; Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1996

C; Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 prot

F; 14-155/Domain: alkyl hydroperoxidase c22 protein homology <C22>

Query Match 16.9%; Score No. 2; Length 200;
Best Local Similarity 31.4%; Pred. No. 7.3e-11;
Matches 59; Conservative 32; Mismatches 85; Indels 12; Gaps 6;

Qy 3 LNLGDSFPDFOAEALGAHEF---RLHEYLGDSGWFMFSHPNDFTPVCTTELAEAVKLQDS 59
Db 5 LRVGQPAPDTTATAIVQSQTVKLSYRG-KYLVLFFYPFLDFTFCPTETIIAFSDRHS 63

Qy 60 PTKKNCKLVGFSCNDLQSHREWAKDIWAYAGRSGLNPFPPLVCPDNRELASLGIMDPK 119
Db 64 FTALDTEWGISVDSEPSHLAWIQTERKMGG-IGNINYPVLVSCLKKEISOAYNVLEP--- 119

Qy 120 DKKGLP LTCRVRFPISEPDKLAASILPATTTGRNFARILRVLDLSQLTAKF--VATPDVM 178
Db 120 -DAGIAL--RGLFIDREGILOIYATVNNSFGSRSVDETLRVLKAIRHVQHSPNEVCPCDV 176

Qy 179 TAGAKCCV 186
Db 177 QEGDKTWI 184

RESULT 37

E87164

A; Title: Mass gene decay in the leprosy bacillus.

C; Species: Mycobacterium leprae

C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C; Accession: E87164

R; Cole, S.T.; Eigilmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho-

R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A; Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; So

A; Title: Massive gene decay in the leprosy bacillus.

A; Reference number: A86909; MUID: 21128732; PMID: 11234002

A; Accession: E87164

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-195 <STO>

A; Cross-references: UNIPROT-Q9CBF5; GB: AL450380; NID: gl3093656; PIDN:CAC30997.1; GSFD:

G; Genetics:

A; Gene: ahpc

C; Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 pro

Query Match 16.7%; Score 199.5; DB 2; Length 195;
Best Local Similarity 29.4%; Pred. No. 1.2e-10;
Matches 53; Conservative 33; Mismatches 63; Indels 31; Gaps 6;

Qy 3 LNLGDSFPDFOAEAL-GAEPRLH-EVLGD-----SWGVMFSSHPNDFTPVCTT 48
Db 4 LSICQQPPAYQTALIIGDSLKSQAQQPGDYFTTVSSDSPGKWVRVVFWPKDFTCIPT 63

Qy 49 ELBAEAVKLQDSFTKKCNKLVGFSCNDLQSHREW---KDIMA VAGRSGNI PFPLVCDPNR 105
Db 64 EI AA FGKLN EF EG GR GA I LG VS ID SE VF HFQWR AQ HD LK ----- RL PP FM L SD IKR 116

Qy 106 ELAASLGIMDPKADKKGLP LTCRVCFPI SPEKKLASILIYPATTGNFAELIRVLDLSQ 165
Db 117 ELSAASGALNAD-----GVADRVTIVDPNDIQVFSTAGS VGRNGVEEVLRVLDAQ 169

RESULT 38

G71492

probable thio-specific antioxidant (tsa) peroxidase - Chlamydia trachomatis (serotype D

C:Species: Chlamydia trachomatis

C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004

C:Accession: G71492

R:Stephens, R.S.; Kalnan, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell

Science 282, 754-759, 1998

A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra

A:Reference number: A71570; MUID:9900809; PMID:9784136

A:Accession: G71492

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-195 <ARN>

A:CROSS-references: UNIPROT:O84608; GB:AE001331; GB:AE001273; NID:G3329046; PIDN:AA0682

A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: ahpC

C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 pro

F:12-153/Domain: alkyl hydroperoxidase c22 protein homology <C22>

Query Match 16.5%; Score 197.5; DB 2; Length 195;

Best Local Similarity 29.0%; Pred. No. 1.1e-10;

Matches 54; Conservative 40; Mismatches 73; Indels 19; Gaps 8;

QY 5 LGDSPDQAEAL--GAE-HFRLEHYLGSGWGFHPNDFTPVCTTEL-AEAVKQDSF 60

DB 5 VGRQAPDFSGKAVCGEEKEISLADFRG-KYVVLFFPKDFTYVCTELHAFQDLVD-F 62

QY 61 TKKNCKLGFVSCNDLQSHREWARDIMAYAGRSNGL---PPFLVCDPNRELASLGIMDPA 117

DB 63 EERGAVWLGSVDYDIETHSRW---LAVARNAGGIEGTVEPLLADPSFKISEAFGLNPE 118

QY 118 EKDKKGLPLTCRCVFFISPEKKLAASILPATYGRNFAEILRVLDLSLQTLAKFPATPVD 177

DB 119 GS-----LALRATFLIDKYGVVRHVINDLPLGRSIDELRIILDSLIFFENHGMVCPAN 172

QY 178 WTAGAK 183

DB 173 WRSGER 178

RESULT 39

C64715

alkyl hydroperoxide reductase (EC 1.6.4.-) - Helicobacter pylori (strain 26695)

N:Alternate names: 26K antigen

C:Species: Helicobacter pylori

C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C:Accession: C64715; A33168

R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenn

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L

Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; MUID:97394467; PMID:9252185

A:Accession: C64715

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-198 <TOM>

A:CROSS-references: UNIPROT:P21762; GB:AE000654; GB:AE000511; NID:G2314743; PIDN:AA0861

R:O'Toole, P.W.; Logan, S.M.; Kostryznska, M.; Wadstroem, T.; Trust, T.J.

J. Bacteriol. 173, 505-513, 1991

A:Title: Isolation and biochemical and molecular analyses of a species-specific protein

A:Reference number: A33168; MUID:91100336; PMID:1987145

A:Accession: A33168

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-35, 'V', 37-63, 'H', 65-97, 'S', 99-198, 'ACLVQDSRSGPGTTELEFVIMVIAVSCVKLLSAHNSTQH

A:CROSS-references: GB:M55507

C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 pro

Keywords: Oxidoreductase
F10-153/Domain: alkyl hydroperoxidase c22 protein homology <C22>

Query Match	16.4%;	Score 195.5;	DB 2;	Length 198;
Best Local Similarity	29.6%;	Pred. No. 2.8e-10;		
Matches 53;	Conservative 28;	Mismatches 85;	Indels 13;	Gaps 4;
QY	10	PDFQAEALG-----AEHFRLHEYLGDSWGVMFSPNDFTPVCTTELAEAVKLQDSFTKKN	64	
Db	8	PDFKAPAVLGNNEVDEHFELSKNLGKNGAILUFWPKOFTFVCPTEIIATDKRVKDFQEK	67	
QY	65	CKLVGSCNDLQSHREWAKDIMAYAGSGNLFPPLVCDPNRELAAIGIMDPAEKDKKL	124	
Db	68	FNIVGISIDSEQVHFAM-KNTPVEKGIGQVTFPMVADITKTSIRDYDLFEE-----	119	
QY	125	PLTCRCVFFTSPEKLAASILYPATTGORNFAEILRVLDLSLQLTAKFPVATPVDMTAGAK	183	
Db	120	AIALRGAFLDIGNKVRHAVINDLPLGRNADEMLRMVDALLHPFEHGEVCPAGRWKGDK	178	

RESULT 40

proliferation associated protein pag homolog, 25k - Japanese common newt
C:Species: Cynops pyrrhogaster (Japanese common newt)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C:Accession: I51016
R;Tabata, T.; Kamio, K.; Tajima, T.; Kaneda, T.; Suzuki, A.
Roux's Arch. Dev. Biol. 204, 400-405, 1995
A:Title: Pag gene-like protein (ASP-25) of Cynops embryo: regional distribution and gene
A:Reference number: I51016
A:Accession: I51016
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-200 <TAB>
A:Cross-references: UNIPROT:Q90384; GB:D37808; NID:G520852; PIDN:BAA07054.1; PID:G520853
C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 prot
F:15-157/Domain: alkyl hydroperoxidase c22 protein homology <C22>

Query Match	16.3%;	Score 195;	DB 2;	Length 200;
Best Local Similarity	30.2%;	Pred. No. 3.1e-10;		
Matches	55;	Conservative 32;	Mismatches 83;	Indels 12; Gaps 6;
QY	5	LGDSFPDFOAEAL--GAE--HFLHEYLGDSWGMRSHPNDFPVCVTTETLAEAVKLODSF	60	
DB	8	IGKPAEFQAKVMPGGEFKDLADYRG-KYVVFPPYPLDFTVCVTEIIAISRDAEEF	66	
QY	61	TKKNCKLVGFSNDLOSHREWAKDIMAYAGRSGNLPPLVLCDPNRELAASLGIMDPAEKD	120	
DB	67	RKINCELIIAASVDSHFCHLAWT-NTSRKEGGLSGMKIPLVADTKRTISQDYGVGL----	121	KE
QY	121	KKGLPLTCRCVFFISPEKKLAASILYPATTTGRNFAETLRVLDSLOLTAKFPVATPVDWTA	180	
DB	122	DEG--ISFRGLFIDDKILRQITINDLPVGRSVDETLRVLQAPQHTDFKFGVCPAGWKP	179	
QY	181	GA	182	
DB	180	GS	181	

Search completed: October 28, 2005, 21:53:33
Job time : 42 secs

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OM protein - protein search, using sw model

Run on: October 28, 2005, 21:53:05 ; Search time 167 Seconds
(without alignments)
558.225 Million cell updates/sec

Title: US-10-723-123-3

Perfect score: 1194

Sequence: 1 MFLNLGDSFPDFOAELGAE.....EALQLPSGKPYLRLTPDRG 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 1865214

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
 - 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
 - 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
 - 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1194	100.0	223	17 US-10-723-123-3	Sequence 3, Appli
2	707	59.2	224	17 US-10-732-923-21412	Sequence 21412, A
3	669.5	56.1	224	17 US-10-732-923-21334	Sequence 21334, A
4	653.5	54.7	224	9 US-09-728-914-37	Sequence 37, Appl
5	653.5	54.7	224	17 US-10-732-923-21440	Sequence 21440, A
6	645.5	54.1	224	17 US-10-732-923-21438	Sequence 21438, A
7	644	53.9	220	17 US-10-732-923-21431	Sequence 21431, A
8	640.5	53.6	224	9 US-09-819-505-4	Sequence 4, Appli
9	640.5	53.6	224	17 US-10-732-923-21327	Sequence 21327, A
10	640.5	53.6	224	17 US-10-732-923-21328	Sequence 21328, A
11	640.5	53.6	235	17 US-10-732-923-21415	Sequence 21415, A

12	638.5	53.5	224	9 US-09-728-914-38	Sequence 38, Appli
13	638.5	53.5	224	9 US-09-819-505-2	Sequence 2, Appli
14	638.5	53.5	224	9 US-09-981-353-4	Sequence 4, Appli
15	638.5	53.5	224	14 US-10-205-823-198	Sequence 198, App
16	638.5	53.5	224	16 US-10-851-921-16	Sequence 16, Appli
17	638.5	53.5	224	17 US-10-502-279-8	Sequence 8, Appli
18	638.5	53.5	224	17 US-10-651-056-3	Sequence 3, Appli
19	638.5	53.5	224	17 US-10-732-923-21433	Sequence 21433, A
20	638.5	53.5	224	20 US-11-051-454-198	Sequence 198, App
21	636	53.3	220	17 US-10-732-923-21325	Sequence 21325, A
22	634.5	53.1	224	17 US-10-732-923-21329	Sequence 21329, A
23	630.5	52.8	224	17 US-10-732-923-21434	Sequence 21434, A
24	626.5	52.5	224	17 US-10-732-923-21330	Sequence 21330, A
25	625.5	52.4	217	17 US-10-732-923-21202	Sequence 21202, A
26	619.5	51.9	219	17 US-10-732-923-21255	Sequence 21255, A
27	619	51.8	221	9 US-09-728-914-2	Sequence 2, Appli
28	619	51.8	221	17 US-10-732-923-21259	Sequence 21259, A
29	618.5	51.8	235	17 US-10-732-923-21419	Sequence 21419, A
30	617.5	51.7	235	9 US-09-728-914-39	Sequence 39, Appli
31	617.5	51.7	235	17 US-10-732-923-21418	Sequence 21418, A
32	609.5	51.0	222	17 US-10-732-923-21155	Sequence 21155, A
33	607.5	50.9	224	17 US-10-732-923-21331	Sequence 21331, A
34	599	50.2	232	17 US-10-732-923-21416	Sequence 21416, A
35	595.5	49.9	249	17 US-10-732-923-21349	Sequence 21349, A
36	588	49.2	222	17 US-10-732-923-21422	Sequence 21422, A
37	588	49.2	222	17 US-10-732-923-21423	Sequence 21423, A
38	587	49.2	222	20 US-11-097-143-5670	Sequence 5670, Ap
39	587	49.2	222	17 US-10-732-923-21424	Sequence 21424, A
40	575	48.2	216	17 US-10-732-923-21413	Sequence 21413, A
41	572.5	47.9	219	17 US-10-732-923-21118	Sequence 21118, A
42	535.5	44.8	219	17 US-10-732-923-21387	Sequence 21387, A
43	533	44.6	250	15 US-10-424-599-206910	Sequence 206910, A
44	529	44.3	222	16 US-10-767-701-45566	Sequence 45566, A
45	521.5	43.7	248	17 US-10-732-923-21350	Sequence 21350, A

ALIGNMENTS

RESULT 1
US-10-723-123-3
; Sequence 3, Application US/10723123
; Publication No. US20050037020A1
; GENERAL INFORMATION:
; APPLICANT: Akzo Nobel N.V.
; TITLE OF INVENTION: Coccidiosis vaccines
; NUMBER OF SEQUENCES: 41
; STREET: Velperweg 76
; CITY: Arnhem
; COUNTRY: The Netherlands
; ZIP: 6824 BM
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/723,123
; FILING DATE: 26-Nov-2003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 0412 666379
; TELEFAX: 0412 650592
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-723-123-3

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Query Match      100.0%; Score 1194; DB 17; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.7e-126;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPLNLGDSFFDQAEALGAHFRHLHEYLGDGSGWMFESHNDFTPVCTTTELAEAVKLQDSF 60
DB 1 MPLNLGDSFFDQAEALGAHFRHLHEYLGDGSGWMFESHNDFTPVCTTTELAEAVKLQDSF 60

QY 61 TKKNCKLVGFSNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPAEKD 120
DB 61 TKKNCKLVGFSNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPAEKD 120

QY 121 KKGGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRLVDSLQLTAKFPVATPDWTA 180
DB 121 KKGGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRLVDSLQLTAKFPVATPDWTA 180

QY 181 GAKCCVVPNLAAEAEQRLPKGHEALQLPSPGKPYLRLTPDP 223
DB 181 GAKCCVVPNLAAEAEQRLPKGHEALQLPSPGKPYLRLTPDP 223

RESULT 2
US-10-732-923-21412
; Sequence 21412, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 21412
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Toxoplasma gondii
; US-10-732-923-21412

Query Match      59.2%; Score 707; DB 17; Length 224;
Best Local Similarity 57.0%; Pred. No. 2.9e-71;
Matches 126; Conservative 36; Mismatches 57; Indels 2; Gaps 1;

QY 3 LNLGDSFFDQAEALG--ABHFRHLHEYLGDGSGWMFESHNDFTPVCTTTELAEAVKLQDSF 60
DB 2 LVLGSTPPDVHADASGVFGDKIKLYDPLGDSWGLMSHPHDFTPVCTTTELAAQARMAPEF 61

QY 61 TKKNCKLVGFSNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPAEKD 120
DB 62 AKRCKLIGFSCDDVSHKGWAKDVMSAKLSGDLPPPIADPERKLTADLQIMDPEEKD 121

QY 121 KKGGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRLVDSLQLTAKFPVATPDWTA 180
DB 122 KAGIPVTCRAAIYIGPDRRVKGLILYPATVGRNFKEVLRALDQLAEKYPVATPEGWFP 181

QY 181 GAKCCVVPNLAAEAEQRLPKGHEALQLPSPGKPYLRLTPDP 221
DB 182 GDKVMVQPTLTDEAKAKLPKGFKEKCPGSKNYLRYAPDP 222

RESULT 3
US-10-732-923-21334
; Sequence 21334, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
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; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 21334
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-732-923-21334

Query Match      56.1%; Score 669.5; DB 17; Length 224;
Best Local Similarity 58.0%; Pred. No. 5.2e-67;
Matches 131; Conservative 29; Mismatches 59; Indels 7; Gaps 4;

QY 1 MP--LNLGDSFFDQAE--ALGAHFRHLHEYLGDGSGWMFESHNDFTPVCTTTELAEAVKLQ 57
DB 1 MPGLLLGDEAPNFEANTTIG--HTRFHDYFLGDSWGLFESHPRDFTPVCTTTELGRAAKLA 58

QY 58 DSFTTKNCKLVGFSNDLQSHREWAKDIMAYAGR--SGNLPPLVCDPNRELAASLGIMD 115
DB 59 PEFAKENVKIALSIDSVEDHFAWSKDINAYNGAAPEKLPFIIDDKORDLAILLGMLD 118

QY 116 PAKDKKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRLVDSLQLTAKFPVATP 175
DB 113 PAKDEKGMPTARVVFIIGPKKLLKLSILYPATTGRNFDILRVVDSLQLTASNVPVATP 178

QY 176 VDWTAGAKCCVVPNLAAEAEQRLPKGHEALQLPSPGKPYLRLTPDP 221
DB 179 VDWKNGESVWVLPTLPEEBAKQLFPKGVFTKELPSGKYLRYTPQ 224

RESULT 4
US-09-728-914-37
; Sequence 37, Application US/09728914
; Patent No. US2001004699A1
; GENERAL INFORMATION:
; APPLICANT: KANTOR, FRED S.
; APPLICANT: FIKRIG, EROL
; APPLICANT: DAS, SUBRATA
; TITLE OF INVENTION: TICK ANTIGENS AND COMPOSITIONS AND METHODS COMPRISING
; TITLE OF INVENTION: THEM
; FILE REFERENCE: YU-107
; CURRENT APPLICATION NUMBER: US/09/728,914
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/169,048
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/240,716
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Bovine sp.
US-09-728-914-37

Query Match      54.7%; Score 653.5; DB 9; Length 224;
Best Local Similarity 56.6%; Pred. No. 3.4e-65;
Matches 128; Conservative 30; Mismatches 61; Indels 7; Gaps 4;

QY 1 MP--LNLGDSFFDQAE--ALGAHFRHLHEYLGDGSGWMFESHNDFTPVCTTTELAEAVKLQ 57
DB 1 MPGLLLGDEAPNFEANTTIG--RIRFHDYFLGDSWGLFESHPRDFTPVCTTTELGRAAKLA 58

QY 58 DSFTTKNCKLVGFSNDLQSHREWAKDIMAYAGR--SGNLPPLVCDPNRELAASLGIMD 115
DB 59 PEFAKENVKIALSIDSVEDHFAWSKDINAYNGEETPEKLPFIIDDKORDLAILLGMLD 118

QY 116 PAKDKKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRLVDSLQLTAKFPVATP 175
DB 119 PAKDEKGMPTARVVFIIGPKKLLKLSILYPATTGRNFDILRVVDSLQLTAKRVATP 178

QY 176 VDWTAGAKCCVVPNLAAEAEQRLPKGHEALQLPSPGKPYLRLTPDP 221
DB 179 VDWKNGDSVWVLPTIPEEBAKQLFPKGVFTKELPSGKYLRYTPQ 224
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RESULT 5
US-10-732-923-21440
; Sequence 21440, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 21440
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-732-923-21440

Query Match      54.7%; Score 653.5; DB 17; Length 224;
Best Local Similarity 56.6%; Pred. No. 3.4e-65;
Matches 128; Conservative 30; Mismatches 61; Indels 7; Gaps 4;

Qy 1 MP--LNLGDSPPDQAE-ALGAEHRLHEYLGDGSGWFMFHPNDFTPVCTTTELAEAVKLQ 57
Db 1 MPGLLLGDEAPNFEANTTIG--RIRFHDVLGDSWGLFSGHPRDFTPVCTTTELGRAAKLA 58

Qy 58 DSFTKKNCKLVGFSNCDLQSHREWAKDIMAYAGR--SGNLPPPLVCDPNRELAASLGIMD 115
Db 59 PEFKRVNVMKIALSDSVDEHLAWSKDINAYNGEETKLPFFPIIDDKNRDLAIQLGMLD 118

Qy 116 PAEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATP 175
Db 119 PAEKDEKGMPTARVVFIFGDKKLLSILYPATTGRNFDLILRVLSQLTAEKRVATP 178

Qy 176 VDMTAGKCCVVPNLAAEEAQRLLPKGHEALQLPSGKPYRLTDPD 221
Db 179 VDMKNGDSVMVLPITPEEAKLPFGKGVFTKELPSGKKYLRYTPQP 224

RESULT 6
US-10-732-923-21438
; Sequence 21438, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 21438
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-732-923-21438

Query Match      54.1%; Score 645.5; DB 17; Length 224;
Best Local Similarity 55.8%; Pred. No. 2.8e-64;
Matches 126; Conservative 32; Mismatches 61; Indels 7; Gaps 4;

Qy 1 MP--LNLGDSPPDQAE-ALGAEHRLHEYLGDGSGWFMFHPNDFTPVCTTTELAEAVKLQ 57
Db 1 MPGLLLGDEAPNFEANTTIG--RIRFHDVLGDSWGLFSGHPRDFTPVCTTTELGRAAKLA 58

Qy 58 DSFTKKNCKLVGFSNCDLQSHREWAKDIMAYAGR--SGNLPPPLVCDPNRELAASLGIMD 115
Db 59 PEFKRVNVMKIALSDSVDEHLAWSKDINAYNGEETKLPFFPIIDDKNRDLAIQLGMLD 118

Qy 116 PAEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATP 175
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Db 119 PAEKDEKGMPTARVVFIFGDKKLLSILYPATTGRNFDLILRVLSQLTAEKRVATP 178

Qy 176 VDMTAGKCCVVPNLAAEEAQRLLPKGHEALQLPSGKPYRLTDPD 221
Db 179 VDMKNGDSVMVLPITPEEAKLPFGKGVFTKELPSGKKYLRYTPQP 224

RESULT 7
US-10-732-923-21431
; Sequence 21431, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 21431
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Plasmodium yoelii yoelii
US-10-732-923-21431

Query Match      53.9%; Score 644; DB 17; Length 220;
Best Local Similarity 56.7%; Pred. No. 4e-64;
Matches 123; Conservative 31; Mismatches 61; Indels 2; Gaps 2;

Qy 1 MPLNLGDSPPDQAEALGAE-HFRLHEYLGDGSGWFMFHPNDFTPVCTTTELAEAVKLQDS 59
Db 1 MGVLGATFPNFATKASGIDGDFELYKIENSNAILFESHHPNDFTPVCTTTELAEGLKKHED 60

Qy 60 FTKKNCKLVGFSNCDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPAEK 119
Db 61 FLKLNCKLVGFSNCKSHDKWIEDI-KYGLKNKWEIPVCDSERELANKLIMDEQEK 119

Qy 120 DKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPDWT 179
Db 120 DITGLPLTCRCVFFISPEKKIKATVLYPATYATGNAHEILRVLSQLTATYTPVATPVNWN 179

Qy 180 AGAKCCVVPNLAAEEAQRLLPKGHEALQLPSGKPYLR 216
Db 180 EGDKCCVIFTLQDDEISKHFKEITKVMESPKKKYL 216

RESULT 8
US-09-819-505-4
; Sequence 4, Application US/09819505
; Patent No. US20020142417A1
; GENERAL INFORMATION:
; APPLICANT: Paigen, Beverly
; Beier, David R.
; TITLE OF INVENTION: Antioxidant Protein 2, Gene and Methods
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: P. O. Box 959
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/819,505
; FILING DATE: 28-Mar-2001
```


Db 67 NVKLGSLSCDSVQSHRWADIIELCRMKSGDSNCCSGNKLPPPIIADNRSLSKLG 126
Qy 114 MDPAEKKGGLPLTCRCVFFISPEKKLAASILYPATTGRNFAETLRVLDLSQLTAKPPVA 173
Db 127 MDPECEDEKGAALTARCLFIIGPKETLKLILYPATTGRNFDLIRVVDLSQLTATKLVA 186
Qy 174 TPVDWTAGAKCCVVPNLAEEAQRLLPKGHEALQLPSGKPYLRLTDP 222
Db 187 TPVDWQNGDDCVVPTINDNEAKLFGKINTVELPSGKPYLRVVAHPK 235

RESULT 12
US-09-728-914-38
; Sequence 38, Application US/09728914
; Patent No. US20010046499A1
; GENERAL INFORMATION:
; APPLICANT: KANTOR, FRED S.
; APPLICANT: FIKRIG, EROL
; APPLICANT: DAS, SUBRATA
; TITLE OF INVENTION: TICK ANTIGENS AND COMPOSITIONS AND METHODS COMPRISING
; FILE REFERENCE: YU-107
; CURRENT APPLICATION NUMBER: US/09/728,914
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/169,048
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/240,716
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-728-914-38

Query Match 53.5%; Score 638.5; DB 9; Length 224;
Best Local Similarity 56.4%; Pred. No. 1.7e-63;
Matches 127; Conservative 28; Mismatches 65; Indels 5; Gaps 3;
Qy 1 MP--LNLGDSFPDFOAEALGAEHFRLHEYLGDSDGVMFSDHPNDFTPVCTTTELAEAVKLQD 58
Db 1 MPGLLLGDVAPNFEANTT-VGRIRPHDFLDGSDGILFSDHPDFTPVCTTTELGRAAKLAP 59
Qy 59 SFTKKNCKLVGFCSDNDLQSHREWAKDIMAY--AGRSNLPPLVCDNRELAAASLGIMDP 116
Db 60 EFARNVKKLIALSDSVEDHLAWSKDINAYNCEBTEKLPFPFIIDDRNRELAILLGLMDP 119
Qy 117 AEKDKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAETLRVLDLSQLTAKPPVATPV 176
Db 120 AEKDEKMPVTARVVFVFGDPKKLKLILYPATTGRNFDLIRVVISQLTAEKRVATPV 179
Qy 177 DWTAGAKCCVVPNLAEEAQRLLPKGHEALQLPSGKPYLRLTDP 221
Db 180 DWKDGDSVMVLPITPEEAKLFPKGVFTKELPSGKKYLYRTPQ 224

RESULT 13
US-09-819-505-2
; Sequence 2, Application US/09819505
; Patent No. US20020142417A1
; GENERAL INFORMATION:
; APPLICANT: Paigen, Beverly
; TITLE OF INVENTION: Antioxidant Protein 2, Gene and Methods
; of Use Therefor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Farrell & Associates
; STREET: P. O. Box 999
; CITY: York Harbor
; STATE: ME

COUNTRY: USA
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/819,505
FILING DATE: 28-Mar-2001
CLASSIFICATION: UNKNOWN
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: JL-2001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-819-505-2

Query Match 53.5%; Score 638.5; DB 9; Length 224;
Best Local Similarity 56.4%; Pred. No. 1.7e-63;
Matches 127; Conservative 28; Mismatches 65; Indels 5; Gaps 3;
Qy 1 MP--LNLGDSFPDFOAEALGAEHFRLHEYLGDSDGVMFSDHPNDFTPVCTTTELAEAVKLQD 58
Db 1 MPGLLLGDVAPNFEANTT-VGRIRPHDFLDGSDGILFSDHPDFTPVCTTTELGRAAKLAP 59
Qy 59 SFTKKNCKLVGFCSDNDLQSHREWAKDIMAY--AGRSNLPPLVCDNRELAAASLGIMDP 116
Db 60 EFARNVKKLIALSDSVEDHLAWSKDINAYNCEBTEKLPFPFIIDDRNRELAILLGLMDP 119
Qy 117 AEKDKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAETLRVLDLSQLTAKPPVATPV 176
Db 120 AEKDEKMPVTARVVFVFGDPKKLKLILYPATTGRNFDLIRVVISQLTAEKRVATPV 179
Qy 177 DWTAGAKCCVVPNLAEEAQRLLPKGHEALQLPSGKPYLRLTDP 221
Db 180 DWKDGDSVMVLPITPEEAKLFPKGVFTKELPSGKKYLYRTPQ 224

RESULT 14
US-09-981-353-4
; Sequence 4, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 3200830CD1
US-09-981-353-4

Query Match 53.5%; Score 638.5; DB 9; Length 224;
Best Local Similarity 56.4%; Pred. No. 1.7e-63;
Matches 127; Conservative 28; Mismatches 65; Indels 5; Gaps 3;

Qy	1	MP--LNLGDSFPDQAEALGABEHFLRHHYFLGDSGWGVMFSPHNDPTPVCTTTELAEAVKLOD	58
Db	1	MPGGLLGLDGVAPNEFANTT-VGRIRFHDFLGDSGWILFSPHNDPTPVCTTTELGRAAKLAP	59
Qy	59	SFTKKNKLVGSCNDLQSHREAWKDINAY--AGRSGNLPPVLVCDNRNRELAISGIMDP	116
Db	60	EFAKRVNKLTAISDSVEDHLAWSKDINAYNCBETKLPFPIIDDRNRELATLLGMDLP	119
Qy	117	AEKDKKGLPLTRCVRFFTSPEKKLAASILYPATTGRNFAETLRVLDLSLOLTAKFPVATPV	176
Db	120	AEKDEKMPVATRVVFVEGPDKKLKLILYPATTGRNFDELLRVVISLOLTAEKRVATPV	179
Qy	177	DWTAGAKCCVVPNLAAEAQRLLPKGHEALQLPSGKPYLRLTDPD	221
Db	180	DWKDGSVMVLPTPIEEAKKLPFGVFTKSLPSGKLYRVTPOD	224

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RESULT 15
US-10-205-823-198
; Sequence 198, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Womsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-198

```

[illegible]

RESULT 17
US-10-502-279-8
Sequence 8, Application US/10502279
Publication No. US2005008480A1
GENERAL INFORMATION:
APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
APPLICANT: Hideki ENDOH
APPLICANT: Ryosuke NAKANO
APPLICANT: Eiji KUROSAKI
APPLICANT: Miyuki KATO
APPLICANT: Hiroyuki YOKOTA
APPLICANT: Kazumori INABE
TITLE OF INVENTION: METHOD FOR SCREENING A DRUG AMELIORATING INSULIN RESISTANCE
FILE REFERENCE: 082704
CURRENT APPLICATION NUMBER: US/10/502,279
CURRENT FILING DATE: 2004-07-23
PRIOR APPLICATION NUMBER: JP 2002-013721
PRIOR FILING DATE: 2002-01-23
PRIOR APPLICATION NUMBER: JP 2002-257703
PRIOR FILING DATE: 2002-09-03
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 224
TYPE: PRT

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; ORGANISM: Homo sapiens
US-10-502-279-8

Query Match
Best Local Similarity 53.5%; Score 638.5; DB 17; Length 224;
Matches 127; Conservative 28; Mismatches 65; Indels 5; Gaps 3;

QY 1 MP--LNLGDSPPDQAEALGAHRLHEYLGDSDGVMFSDHNDPTPVCTTELAEAVKLQD 58
Db 1 MPGLLLGDVAPNEANTT-VGRIRFHDFLGDSWGILFSDHNDPTPVCTTELGRAAKLAP 59

QY 59 SFTKKNCKLVGFSNDLQSHREWAKDIMAY--AGRSNLPPLVCDPNRELAASLGIMDP 116
Db 60 EFARNVKLIALSIDSVEDHLAWSKDINAYNCEBTEKLPPIIDRRNRELAAILGLMDP 119

QY 117 AEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAELRLVLDLSQLTAKFPVATPV 176
Db 120 AEKDEKGMPTARVVFVFGPKLKLILYPATTGRNFAELRLVLDLSQLTAKFPVATPV 179

QY 177 DWTAGAKCCVVPNLAAEAQRLPKGHEALQLPSGKPYRLRTPDP 221
Db 180 DWKDGSDVMVLPTIPEEAKKLPKGVFTKELPSGKKYLRYTPQP 224

RESULT 18
US-10-651-056-3
; Sequence 3, Application US/10651056
; Publication No. US20050100979A1
; GENERAL INFORMATION:
; APPLICANT: POWER, John Henry Thomas
; TITLE OF INVENTION: METHODS FOR DETECTING OXIDATIVE STRESS
; FILE REFERENCE: 0641-0254P
; CURRENT APPLICATION NUMBER: US/10/651,056
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-651-056-3

Query Match
Best Local Similarity 53.5%; Score 638.5; DB 17; Length 224;
Matches 127; Conservative 28; Mismatches 65; Indels 5; Gaps 3;

QY 1 MP--LNLGDSPPDQAEALGAHRLHEYLGDSDGVMFSDHNDPTPVCTTELAEAVKLQD 58
Db 1 MPGLLLGDVAPNEANTT-VGRIRFHDFLGDSWGILFSDHNDPTPVCTTELGRAAKLAP 59

QY 59 SFTKKNCKLVGFSNDLQSHREWAKDIMAY--AGRSNLPPLVCDPNRELAASLGIMDP 116
Db 60 EFARNVKLIALSIDSVEDHLAWSKDINAYNCEBTEKLPPIIDRRNRELAAILGLMDP 119

QY 117 AEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAELRLVLDLSQLTAKFPVATPV 176
Db 120 AEKDEKGMPTARVVFVFGPKLKLILYPATTGRNFAELRLVLDLSQLTAKFPVATPV 179

QY 177 DWTAGAKCCVVPNLAAEAQRLPKGHEALQLPSGKPYRLRTPDP 221
Db 180 DWKDGSDVMVLPTIPEEAKKLPKGVFTKELPSGKKYLRYTPQP 224

RESULT 19
US-10-732-923-21433
; Sequence 21433, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10

; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 21433
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-923-21433

Query Match
Best Local Similarity 53.5%; Score 638.5; DB 17; Length 224;
Matches 127; Conservative 28; Mismatches 65; Indels 5; Gaps 3;

QY 1 MP--LNLGDSPPDQAEALGAHRLHEYLGDSDGVMFSDHNDPTPVCTTELAEAVKLQD 58
Db 1 MPGLLLGDVAPNEANTT-VGRIRFHDFLGDSWGILFSDHNDPTPVCTTELGRAAKLAP 59

QY 59 SFTKKNCKLVGFSNDLQSHREWAKDIMAY--AGRSNLPPLVCDPNRELAASLGIMDP 116
Db 60 EFARNVKLIALSIDSVEDHLAWSKDINAYNCEBTEKLPPIIDRRNRELAAILGLMDP 119

QY 117 AEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAELRLVLDLSQLTAKFPVATPV 176
Db 120 AEKDEKGMPTARVVFVFGPKLKLILYPATTGRNFAELRLVLDLSQLTAKFPVATPV 179

QY 177 DWTAGAKCCVVPNLAAEAQRLPKGHEALQLPSGKPYRLRTPDP 221
Db 180 DWKDGSDVMVLPTIPEEAKKLPKGVFTKELPSGKKYLRYTPQP 224

RESULT 20
US-11-051-454-198
; Sequence 198, Application US/11051454
; Publication No. US20050191673A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/11/051,454
; CURRENT FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: US/10/205,823
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-454-198

Query Match
Best Local Similarity 53.5%; Score 638.5; DB 20; Length 224;
```


Db 64 KKNVKGIGLSDASDSASHKWDIIALYKMKVCVGCDSKKLPYPYIADDESRSLATEGM 123
QY 114 MPAEKDKKGLPITCRVFFISPEKKLAASILYPATTGRNFAELRLVDSLQLTAKFPVA 173
Db 124 MDPDERDEKNTLTARCVFIIGSDKTLKLSILYPATTGRNFEILRAVDSLQLTAVKVA 183
QY 174 TPVDWTAGAKCCVVPNLAAEEAQRLLPKGHEALQLPSCGPYLRITPDP 222
Db 184 TPVDWKDGDGVVLTIDNEAKKJFGEKIHTIDLPFGKHLYRMVPHPK 232

RESULT 35

US-10-732-923-21349
; Sequence 21349, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 21349
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Anopheles gambiae str. PEST
US-10-732-923-21349

Query Match 49.9%; Score 595.5; DB 17; Length 249;
Best Local Similarity 52.7%; Pred. No. 1.5e-58;
Matches 118; Conservative 28; Mismatches 73; Indels 5; Gaps 3;
QY 1 MFLNLGDSPPDFOAE-ALGAEHRLHEYLGDSDGVMFSGHPNDFTPVCTTTELAEAVKLQDS 59
Db 27 MSNLGDPFPNFADTTIGIDF--HQWIGDGMWILFSDPADFTPVCTTTELAEAVKLVE 84
QY 60 FTKKCKLVGFSNDLQSHREWAKDIMAYA--GRSGNLPFPLVCDPNRELAASLGIMDPA 117
Db 85 FTKRNKPIALSCDVTESHKGWIEDIKAYQLAAADPFPFPIIDDSKRELAVKLNMLDRD 144
QY 118 EKDKKGLPITCRVFFISPEKKLAASILYPATTGRNFAELRLVDSLQLTAKFPVATPD 177
Db 145 EIGSAGLPLTCRAVFVIDAGKKLRLSILYPATTGRNFAELRLTIDSQLTQTKRVATPAD 204
QY 178 WTAGAKCCVVPNLAAEEAQRLLPKGHEALQLPSCGPYLRITPDP 221
Db 205 WMFGDSGMVQTPVPAOQLATLFPAGVDSVTLPSGKQYLRKTECP 248

RESULT 36

US-10-732-923-21422
; Sequence 21422, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 21422
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-732-923-21422

Query Match 49.2%; Score 588; DB 17; Length 222;
Best Local Similarity 49.3%; Pred. No. 9.1e-58;

Matches 108; Conservative 38; Mismatches 71; Indels 2; Gaps 2;
QY 3 LNLGDSPPDFOAEALGAEHRLHEYLGDSDGVMFSGHPNDFTPVCTTTELAEAVKLQDSFTK 62
Db 6 LNLGQFPNFTAET-SEGRIDFYDMQDSWAILFSDPADFTPVCTTTELSRVAALIFEFOK 64
QY 63 KNCKLVGFSNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPAEKDKK 122
Db 65 RGVKPIALSCDVTESHKGWIEDIKSF-GKLSGFDYPIIADDKRELAKFNMLDKDEINAE 123
QY 123 GLPLTCRCVFFISPEKKLAASILYPATTGRNFAELRLVDSLQLTAKFPVATPDVMTAGA 182
Db 124 GIPLTCRAVFVVDKDKLRLSILYPATTGRNFEILRLVDSLQLTQTKSVATPADWKQGG 183
QY 183 KCCVVPNLAAEEAQRLLPKGHEALQLPSCGPYLRITPDP 221
Db 184 KCWLPTVKAEDVPKLPDGIETIELPSGKSYLRITPQP 222

RESULT 37

US-10-732-923-21423
; Sequence 21423, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 21423
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-732-923-21423

Query Match 49.2%; Score 588; DB 17; Length 222;
Best Local Similarity 49.3%; Pred. No. 9.1e-58;
Matches 108; Conservative 38; Mismatches 71; Indels 2; Gaps 2;
QY 3 LNLGDSPPDFOAEALGAEHRLHEYLGDSDGVMFSGHPNDFTPVCTTTELAEAVKLQDSFTK 62
Db 6 LNLGQFPNFTAET-SEGRIDFYDMQDSWAILFSDPADFTPVCTTTELSRVAALIFEFOK 64
QY 63 KNCKLVGFSNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPAEKDKK 122
Db 65 RGVKPIALSCDVTESHKGWIEDIKSF-GKLSGFDYPIIADDKRELAKFNMLDKDEINAE 123
QY 123 GLPLTCRCVFFISPEKKLAASILYPATTGRNFAELRLVDSLQLTAKFPVATPDVMTAGA 182
Db 124 GIPLTCRAVFVVDKDKLRLSILYPATTGRNFEILRLVDSLQLTQTKSVATPADWKQGG 183
QY 183 KCCVVPNLAAEEAQRLLPKGHEALQLPSCGPYLRITPDP 221
Db 184 KCWLPTVKAEDVPKLPDGIETIELPSGKSYLRITPQP 222

RESULT 38

US-11-097-143-5670
; Sequence 5670, Application US/11097143
; Publication No. US2005020858A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2005, 21:33:02 ; Search time 167 Seconds
(without alignments)
516.452 Million cell updates/sec

Title: US-10-723-123-3
Perfect score: 1194
Sequence: 1 MPLNLGDSPPDFOAALGAE.....EALQLPSGKFLRLTDPDPRG 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseq1980s:.*
2: Geneseq1990s:.*
3: Geneseq2000s:.*
4: Geneseq2001s:.*
5: Geneseq2002s:.*
6: Geneseq2003as:.*
7: Geneseq2003bs:.*
8: Geneseq2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1194	100.0	223	3	AAY79496 Elmeria t
2	669.5	56.1	225	7	Ad48548 Rat Prote
3	669.5	56.1	225	7	Ad48997 Rat Prote
4	668.5	56.0	223	7	Ad48552 Rat Prote
5	668.5	56.0	223	7	Ad54680 Rat Prote
6	641.5	53.7	224	6	Abu07558 Mouse ant
7	640.5	53.6	224	2	Aaw76700 Mouse ant
8	640.5	53.6	224	6	Abu07559 Mouse ant
9	640.5	53.6	235	2	Aaw88274 Brugia ma
10	639.5	53.6	224	6	Abu07557 Human enc
11	638.5	53.5	224	2	Aaw76699 Human ant
12	638.5	53.5	224	6	Adal0886 Human CDN
13	638.5	53.5	224	7	AdB80263 PPARGgamma
14	638.5	53.5	224	7	AdB75374 Prostata
15	638.5	53.5	224	7	Ad48554 Human Pro
16	638.5	53.5	224	8	Ado24813 Human per
17	638.5	53.5	224	8	Adm80206 Tumour-as
18	638.5	53.5	224	8	AdP23043 PRO polyp
19	638.5	53.5	253	4	Aau23423 Novel hum
20	637.5	53.4	223	4	AAB68039 Amino aci
21	637.5	53.4	223	7	Ad48999 Human Pro
22	637.5	53.4	223	7	Ad54682 Human Pro
23	637.5	53.4	223	7	Ad48550 Human Pro
24	619	51.8	221	4	AAY97763 I. scapul
25	618.5	51.8	235	2	AAW88273 Dirofilar

26	609.5	51.0	222	5	AAG66167 Tick pero
27	607.5	50.9	224	6	Abu07560 Mouse ant
28	588	49.2	222	4	AbB59626 Drosophil
29	585	49.0	250	2	AAR34196 O-CSF. 3/
30	507.5	42.5	177	8	ADO24814 Human per
31	507.5	42.5	212	8	AdS24874 Bacterial
32	501.5	42.0	220	4	AbB65897 Drosophil
33	498.5	41.8	220	4	AbB59059 Drosophil
34	497.5	41.7	222	7	ABO68070 Pseudomon
35	495	41.5	218	5	ABB80958 Barley 1-
36	494.5	41.4	212	8	AdN21975 Bacterial
37	494.5	41.4	212	8	AdN24733 Bacterial
38	494.5	41.4	216	6	AdA34041 Acinetoba
39	493.5	41.3	212	8	AdN22014 Bacterial
40	493.5	41.3	212	8	AdN24773 Bacterial
41	492	41.2	211	8	AdN20019 Bacterial
42	486.5	40.7	216	5	ABB80959 A. thalia
43	486.5	40.7	216	6	ABR39572 A. thalia
44	481	40.3	211	8	AdS21318 Bacterial
45	473.5	39.7	212	8	AdN26021 Bacterial

ALIGNMENTS

RESULT 1
AAY79496
ID AAY79496 standard; protein; 223 AA.
XX AC
XX AAY79496;
XX XX
DT 01-AUG-2000 (first entry)
XX XX
DE Elmeria tenella 25 kDa peroxidoxin-like hydrophilic protein.
XX XX
KW Coccidiosis; vaccine; poultry; peroxidoxin.
XX XX
OS Elmeria tenella.
XX XX
PN EP995799-A2.
XX XX
PD 26-APR-2000.
XX XX
PF 01-OCT-1999; 99EP-00203214.
XX XX
PR 07-OCT-1998; 98EP-00203384.
PR 16-OCT-1998; 98EP-00203457.
XX XX
PA (ALKU) AKZO NOBEL NV.
XX XX
PI Schaap TC, Kuijper CM, Vermeulen AN;
XX XX
DR WPI; 2000-305655/27.
N-PSDB; AAZ94936.
XX XX
PT Novel hydrophilic Elmeria polypeptides comprise sequences with at least
70% homology with sequences of 13-223 amino acids, useful as vaccines
against Coccidiosis in poultry.
XX XX
PS Claim 3; Page 3; 30pp; English.
XX XX
CC The present sequence is that of a 25 kDa peroxidoxin-like hydrophilic
protein of Elmeria tenella. The polypeptide was obtained from the
hydrophilic phase of a total sporozoite protein fraction of E. tenella
weybridge strain. The invention provides 6 hydrophilic polypeptides (see
AA79494-99) of Elmeria. These polypeptides, or immunogenic fragments of
them, can be used in vaccines to protect poultry against the pathogenic
effects of Elmeria, the causative agent of intestinal coccidiosis. The
polypeptides are also useful for detecting antibodies against Elmeria
infection in poultry. DNA encoding the polypeptide can be used to detect
Elmeria parasites and as a vaccine, optionally in a live recombinant
carrier

Db	182	KGESVMVLP	TLPEEAKQLFPKGVFTKELPSGKKYLRYTPQP	223	
AD554680					
ID	AD554680	standard; protein; 223 AA.			
AC	AD554680;				
DT	29-JAN-2004	(first entry)			
DE	Rat Protein O35244,	SEQ ID NO 485.			
KW	Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;				
KW	chronic constriction injury; CCI; spared nerve injury; SN1; Chung.				
OS	Rattus norvegicus.				
XX	WO2003016475-A2.				
XX					
PD	27-FEB-2003.				
XX					
PF	14-AUG-2002; 2002WO-US025765.				
XX					
PR	14-AUG-2001; 2001US-0312147P.				
PR	01-NOV-2001; 2001US-0346382P.				
PR	26-NOV-2001; 2001US-0333347P.				
XX					
PA	(GEHO) GEN HOSPITAL CORP.				
PA	(FARB) BAYER AG.				
XX					
PI	Woolf C, D'urso D, Befort K, Costigan M;				
XX					
XX	WPI; 2003-268312/26.				
DR	GENBANK; O35244.				
XX					
FT	New composition comprising two or more isolated polypeptides, useful for				
PT	preparing a medicament for treating pain in an animal.				
XX					
PS	Claim 1; Page; 1017pp; English.				
XX					
CC	The invention discloses a composition comprising two or more isolated rat				
CC	or human polynucleotides or a polynucleotide which represents a fragment,				
CC	derivative or allelic variation of the nucleic acid sequence. Also				
CC	claimed are a vector comprising the novel polynucleotide, a host cell				
CC	comprising the vector, a method for identifying a nucleotide sequence				
CC	which is differentially regulated in an animal subjected to pain and a				
CC	kit to perform the method, an array, a method for identifying an agent				
CC	that increases or decreases the expression of the polynucleotide sequence				
CC	that is differentially expressed in neuronal tissue of a first animal				
CC	subjected to pain, a method for identifying a compound which regulates				
CC	the expression of a polynucleotide sequence which is differentially				
CC	expressed in an animal subjected to pain, a method for identifying a				
CC	compound that regulates the activity of one or more of the				
CC	polynucleotides, a method for producing a pharmaceutical composition, a				
CC	method for identifying a compound or small molecule that regulates the				
CC	activity in an animal of one or more of the polypeptides given in the				
CC	specification, a method for identifying a compound useful in treating				
CC	pain and a pharmaceutical composition comprising the one or more				
CC	polypeptides or their antibodies. The polynucleotide or the compound that				
CC	modulates its activity is useful for preparing a medicament for treating				
CC	pain (e.g. spinal segmental nerve injury (Chung), chronic constriction				
CC	injury (CCI) and spared nerve injury (SN1)) in an animal (e.g. gene				
CC	therapy). The sequence presented is a rat protein (shown in Table 2 of				
CC	the specification) which is differentially expressed during pain. Note:				
CC	The sequence data for this patent did not form part of the printed				
CC	specification, but was obtained in electronic form directly from WIPO at				
CC	ftp.wipo.int/pub/published_pct_sequences.				
XX					
SQ	Sequence 223 AA;				
	Query Match	56.0%;	Score 668.5;	DB 7;	Length 223;

	Best Local Similarity	58.1%;	Pred. No. 1.7e-66;		
	Matches 129;	Conservative	29;	Mismatches	59;
				Indels	5;
				Gaps	3;
OY	3	LNIGDSFPDFOAE-ALGAEHFRLEHYLGDWGMFSGHNDFTPVCTTELAEAVKLQDSPT	61		
Db	4	LLLGDEAPNFEANTTIG--HIFHDFLGDWGLFSHPDFTPVCTTELGRAAKLAPEFA	61		
OY	62	KKNCKLVGFSNDLQSHREWAKDIWAYAGR--SGNLPFPLVCDPNRELAASLGIMDPAEK	119		
Db	62	KKNVKLIALSIDSVDHFAWSKDINAYNGAAPTEKLPFPIIDDKORDLAILLGMLDPAEK	121		
OY	120	DKKGLPLTCRCVFFISPEKLAASILYPATTTCNFAETILRVLDLSQLTAKFPVATPDWMT	179		
Db	122	DEKGMPTVARTVVVIFGPKKKLSILYPATTTCNFAETILRVLDLSQLTAKFPVATPDWMT	181		
OY	180	AGAKCCVVPNLAAEAQRLPKGHEALQPSGKPYLRLTPDP	221		
Db	182	KGESVMVLP	TLPEEAKQLFPKGVFTKELPSGKKYLRYTPQP	223	
RESULT 6					
ABU07558					
ID	ABU07558	standard; protein; 224 AA.			
XX					
AC	ABU07558;				
XX					
DT	18-MAR-2003	(first entry)			
XX					
DE	Mouse antioxidant protein 2, Aop2 #1.				
XX					
KW	Mouse; antioxidant protein 2; Aop2; atherosclerosis; antiatherosclerotic;				
KW	antioxidant; atherosclerotic lesion; oxidative damage; heart surgery;				
KW	SNP; chromosome 1. single nucleotide polymorphism.				
XX					
OS	Mus sp.				
XX					
FT	Key	Location/Qualifiers			
FT	Misc-difference 1.	.224			
FT		/note= "The last letter of the last Amino acid in each			
FT		row has not been reproduced in the specification, the			
FT		indexer has added the correct letter to restore the			
FT		correct 3 letter code except where ambiguity exists (see			
FT		below)"			
FT	Misc-difference 96	/label= OTHER			
FT		/note= "Encoded by GAA, probably Glu, appears as Gl in			
FT		the specification"			
FT	Misc-difference 124				
FT		/note= "May be Asp as the result of a single nucleotide			
FT		polymorphism"			
XX					
PN	US2002142417-A1.				
XX					
PD	03-OCT-2002.				
XX					
PF	28-MAR-2001; 2001US-00819505.				
XX					
PR	02-APR-1997; 97US-0040898P.				
PR	01-APR-1998; 98US-00053088.				
XX					
PA	(PAIG/) PAIGEN B.				
PA	(BEIE/) BEIER D R.				
XX					
PI	Paigen B, Beier DR;				
XX					
DR	WPI; 2003-155944/15.				
DR	N-PSDB; ABX15202.				
XX					
FT	Novel antioxidant protein-2 polypeptide useful for diagnosing				
PT	predisposition to atherosclerotic lesions in subject, and screening a				
PT	compound for the protein stimulatory activity.				
XX					
PS	Claim 5; Page 39-40; 54pp; English.				

Db 7 LGDKFPDQAESETSEFSSFDHWGKDSWAILFSHPDRDFTVCTTELARLVLEPEFKR 66
Qy 64 NCKLVGFSNCNDLQSHREWAKDIMAYAGR-----SGN-LPPLVCDNRELAAISGI 113
Db 67 NVKLIGLSCDSVQSHRWADDIELCRMKSGDSNTCCSGNKLPPFIADNRSLSAKLGM 126
Qy 114 MDPAEKDKGLPLTCRCVFFISPBKLAASILYPATTGRNFAELRLVDSLSQLTAKFPVA 173
Db 127 MDPDECDEKGAALTARCLFTIGPEKTLKLSILYPATTGRNFDLRLVDSLSQLTATKVA 186
Qy 174 TPVDWTAGKCCVVPNLAABEAQRLPKGHEALQLPSGKPYLRITPPDR 222
Db 187 TPVDWQMGDDCVVPTINDNEAKLFGKINTVLPESGKPYLRVVAHPK 235

RESULT 10
ABU07557
ID ABU07557 standard; protein; 224 AA.
XX AC ABU07557;
XX DT 18-MAR-2003 (first entry)
XX DE Human encoding antioxidant protein 2, Aop2.
XX KW Human; antioxidant protein 2; Aop2; atherosclerosis; antiatherosclerotic;
XX KW antioxidant; atherosclerotic lesion; oxidative damage; heart surgery;
XX KW chromosome 1q23-25.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Misc-difference 1..224
FT /note= "The last letter of the last Amino acid in each
FT row has not been reproduced in the specification, the
FT index has added the correct letter to restore the
FT correct 3 letter code except where ambiguity exists (see
FT below)"
FT Misc-difference 96
FT /label= OTHER
FT /note= "Encoded by GAA, probably Glu, appears as Gl in
FT the specification"
XX US2002142417-A1.
XX 03-OCT-2002.
XX 28-MAR-2001; 2001US-00819505.
XX 02-APR-1997; 97US-0040898P.
XX 01-APR-1998; 98US-00053088.
XX (PAIG/) PAIGEN B.
XX (BEIE/) BEIER D R.
XX Paigen B, Beier DR;
XX WPI; 2003-155944/15.
XX N-PSDB; ABX15201.
XX Novel antioxidant protein-2 polypeptide useful for diagnosing
XX predisposition to atherosclerotic lesions in subject, and screening a
XX compound for the protein stimulatory activity.
XX Claim 4; Page 38; 54pp; English.
XX The invention relates to an isolated antioxidant protein-2 polypeptide,
XX designated Aop2, its antigenic fragment or the nucleotide encoding Aop2
XX (Aop2 NA). Also included are Aop2 NA oligonucleotides, screening a
XX compound for AOP2 stimulatory activity, screening a compound for anti-
XX atherosclerotic activity (by providing a lipid, contacting the lipid with
XX a candidate antioxidant, and determining the oxidation state of the
XX lipid), an anti-Aop2 mono/polyclonal antibody, an Aop2 NA expression

CC vector, a host cell comprising Aop2 NA and reducing atherosclerotic
CC lesions in a subject (by administering a lipid antioxidant composition to
CC the subject). Aop2 is useful for diagnosing a predisposition to
CC atherosclerotic lesions in a subject involving determining the
CC antioxidant activity of an Aop2 polypeptide of the sample, or the level
CC of an Aop2 polypeptide in cells of the sample or involves polymerase
CC chain reaction (PCR), and the determining step is performed by contacting
CC the sample with an anti-Aop2 antibody, or determining the sequence of
CC nucleic acid from the sample that encodes an Aop2 polypeptide. Aop2 is
CC also useful for screening a compound for AOP2 stimulatory activity. Aop2
CC NA is useful for increasing AOP2 function in a cell. The expression
CC vector may be a viral vector, encapsulated in a liposome. The viral
CC vector is adenoviral, retroviral, vaccinia, adeno-associated viral
CC vector, or herpes viral vector. The cell is located in a human subject,
CC or an experimental animal. The promoter is cytomegalovirus (CMV), rous
CC sarcoma virus (RSV), or E1A. Aop2 is also useful in preventing oxidative
CC damage in vivo, for e.g., during heart surgery, where blood is oxygenated
CC outside the body. Aop2 or Aop2 NA is useful for treating atherosclerosis.
CC The present sequence represents human Aop2, the gene for which is located
CC on human chromosome 1q23-25
XX
SQ Sequence 224 AA;

Query Match 53.6%; Score 639.5; DB 6; Length 224;
Best Local Similarity 56.4%; Pred. No. 3.2e-63;
Matches 127; Conservative 28; Mismatches 65; Indels 5; Gaps 3;

Qy 1 MP--LNLGSPDPFOAEALGAEHRLHEVLGDSWGMFSPNDFTPVCTTELEAVKLQD 58
Db 1 MPGGLLGDVAPNFEANTT-VGRIRPHDFLGDGWSGLFSHPDRDFTPVCTTELEAAKLAP 59
Qy 59 SFTKKNCKLVGFSNCNDLQSHREWAKDIMAY--AGRSNLPFPPLVCDNRELAAASLGIMDP 116
Db 60 EFAKRVNKLIALSIDSVDEHLAWSKDINAYNCEPTXKLPFIIDNRELAILLGLMDP 119
Qy 117 AEKDKGLPLTCRCVFFISPBKLAASILYPATTGRNFAELRLVDSLSQLTAKFPVATPV 176
Db 120 AEKDEKGMPTARVVFVFGPKKLSILYPATTGRNFDLRLVDSLSQLTAKSRVATPV 179
Qy 177 DWTAGAKCCVVPNLAABEAQRLPKGHEALQLPSGKPYLRITPPDR 221
Db 180 DWKGDGSMVLPFTIPBEEAKKLPFGVFTKELPSGKKYLRVTFQP 224

RESULT 11
AAW76699
ID AAW76699 standard; protein; 224 AA.
XX AC AAW76699;
XX 02-FEB-1999 (first entry)
XX Human antioxidant protein 2 (AOP2).
XX Antioxidant protein 2; AOP2; human; atherosclerosis; Acl1; heart disease;
XX KW diagnosis; therapy; drug screening.
XX OS Homo sapiens.
XX WO9843666-A1.
XX 08-OCT-1998.
XX 01-APR-1998; 98WO-US006666.
XX 02-APR-1997; 97US-0040897P.
XX (JACK-) JACKSON LAB.
XX (BGM) BRIGHAM & WOMENS HOSPITAL.
XX Paigen B, Beier DR;
XX WPI; 1998-568267/48.
DR

XX Endoh H, Nakano R, Kurosaki E, Kato M, Yokota H, Inabe K;
PI WPI; 2003-598753/56.
XX N-PSDB; ADB80262.
XX
PT Screening for proteins that interact with peroxisome proliferator-
PT activated receptor (PPAR) for screening for drugs that improve insulin
PT resistance.
XX
XX Claim 4; Page 96-98; 116pp; Japanese.
PS
PS
XX The invention relates to a method for screening for proteins that
CC interact with peroxisome proliferator-activated receptor-gamma
CC (PPARgamma). The method of the invention is ligand-dependent and
CC comprises using a polynucleotide encoding at least residues 204-505 of a
CC fully defined 505 amino acid sequence as the bait, and a yeast two hybrid
CC system using a cDNA library as prey in the presence of the PPAR ligand.
CC Also disclosed are cells that express the PPAR protein, a method for
CC screening for drugs for insulin resistance, and preparing a medical
CC composition for improving insulin resistance. The method of the invention
CC is useful for screening for drugs that improve insulin resistance. The
CC current sequence represents a PPARgamma related protein.
XX
XX Sequence 224 AA;
SQ

Query Match	53.5%;	Score 638.5;	DB 7;	Length 224;
Best Local Similarity	56.4%;	Pred. No. 4.1e-63;		
Matches 127; Conservative	28;	Mismatches 65;	Indels 5;	Gaps 3;

Qy	1	MP--LNIGDSPDPFAEALGAAEHRLHEYLGDSDGVMFSSHENDTPVCTTLEAAVKLQD	58
		: : : :	
Db	1	MPGCLLLGDVPANPEANTT-VGRIRFHDPLDGDSWGLFSHPERDTPVCTTELGRAAKLAP	59
		: : : :	
Qy	59	SFTKKNCKLVGFSCNDIQLSHREWAQIMAY--AGRSGNLPPPLVCDPNRELAAISIGIMDP	116
		: : : :	
Db	60	EFAKRNVKLIALSIDSVEDHLAWSKDINAYNCEEPTFKLPPIIDDRNRRELAILLGLMDP	119
		: : : :	
Qy	117	AEKDKGLPLTRCVCFFITSPKKLAAASILYPAATGRNFAETLRVLDSLQLTAKEPVATPV	176
		: : : :	
Db	120	AEKDEKMPVTARVVVFVGPDKKLSILIPATTGRNFDELRLRVVISQLTAEKRVATPV	179
		: : : :	
Qy	177	DWTAGAKCCVVVNIAABEAQRLLPKGHEALQLPSGKYRLRUTPPP	221
		: : : :	
Db	180	DWKDGDVSVMVLPPTTPEBAKKLPFGVFTKELPSGKKLYRTPOP	224
		: : : :	

RESULT 14
ADB75374
ID ADB75374 standard; protein: 224 AA.

XX	ADB75374;	
AC		
XX		
DT	04-DEC-2003 (first entry)	
XX		
DE	Prostate cancer marker protein.	
XX		
XX		
KW	Prostate; cancer; cytostatic; gene therapy; marker.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2003009814-A2.	
XX		
PD	06-FEB-2003.	
XX		
PF	25-JUL-2002; 2002WO-US023913.	
XX		
PR	25-JUL-2001; 2001US-0307982P.	
PR	22-AUG-2001; 2001US-0314356P.	
PR	23-SEP-2001; 2001US-0325020P.	
PR	12-DEC-2001; 2001US-0341746P.	
PR	05-MAR-2002; 2002US-0362158P.	
XX		

(MILL-) MILLENNIUM PHARM INC.
 Schlegel R, Monahan JB, Endege WO, Gannavarapu M, Gorbacheva B;
 Hoersh S, Kamatkar S, Wonsey AM, Glatt K, Zhao X, Anderson D;
 WPI; 2003-248033/24.
 New nucleic acid molecule, useful for diagnosing or treating prostate
 cancer.
 Disclosure; SEQ ID NO 198; 99pp; English.
 The invention relates to newly discovered cancer markers associated with
 the cancerous state of prostate cells. Also disclosed is a method of
 assessing whether a patient is afflicted with prostate cancer. The method
 of the invention involves assessing whether a patient is afflicted with
 prostate cancer by comparing the level of expression of a marker in a
 patient sample and the normal level of expression of the marker in a
 control non-prostate cancer sample, where a significant increase in the
 level of expression of the marker in the patient sample and the normal
 level indicates that the patient is afflicted with prostate cancer.
 Nucleic acids of the invention are useful for diagnosing or treating
 prostate cancer, and may be useful in gene therapy. Sequences given in
 ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
 data for this patent did not form part of the printed specification, but
 was obtained in electronic format directly from WIPO at
 ftp.wipo.int/pub/published_pct_sequences.
 Sequence 224 AA;

Query Match	53.5%	Score 638.5	DB 7	Length 224
Best Local Similarity	56.4%	Pred. No. 4.1e-63		
Matches 127	Conservative 28	Mismatches 65	Indels 5	Gaps 3
QY	1	MP- -LNLGDSFPDQAEALCAEHRLHEYLGDGSGVMFSDHNDPTPCTTTELAEAVKLQD	58	
DB	1	MPGGLLGLDVAPNEANTT- -VGRIRHDFGLGDSWGLFSDHPRDPTPCTTTELGRAAKLAP	59	
QY	59	SFTKKNCKLVGFSNDLQSHREWAKDIMAY- -AGRSNLPFPLVCDPNRELAAASLGIMDP	116	
DB	60	EPAKRVNKLIALSIDSVEDHLAWSKDINAYNCEPTEKLPFPFIIDRRNELAILLGLMDP	119	
QY	117	AEKDKGKLPITCRCVFISPEKKLAASILYPATTGRNFAEILRVLDSLQLTAKFPVATPV	176	
DB	120	AEKDEKMPVARTARVVFVFGDPKKLKULYPATTGRNFDIELRVVISLQLTAEKRKATPV	179	
QY	177	DWTAGAKCCVVPNLAAEAEQRLLPKGHEALQLPSPGKPYRLTDPD	221	
DB	180	DWKDGSVMVLPITPISEAAKLLPKGVFTKELPSGKKLYRTPOD	224	

RESULT 15	
ADD48554	
ID	ADD48554 standard; protein; 224 AA.
XX	
AC	ADD48554;
XX	
DT	02-DEC-2004 (revised)
DT	29-JAN-2004 (first entry)
XX	
DE	Human Protein NP_004896, SEQ ID NO 14258.
XX	
XX	Human; pain; neuronal tissue; gene therapy;
KW	spinal segmental nerve injury; chronic constriction injury; CCI;
KW	spared nerve injury; SNI; Chung.
XX	
OS	Homo sapiens.
OS	Unidentified.
XX	
PN	W02003016475-A2.
XX	
PD	27-FEB-2003.
XX	

PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX
PA (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI: 2003-268312/26.
DR GENBANK; NP_004896.
XX
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX
PS Example 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 224 AA;
Query Match 53.5%; Score 638.5; DB 7; Length 224;
Best Local Similarity 56.4%; Pred. No. 4.1e-63;
Matches 127; Conservative 28; Mismatches 65; Indels 5; Gaps 3;
QY 1 MP--LNLGDSFPDFOAEALGAHFRHLHYLGDSWGMFSDHPNDFTPVCTTELAEAVKLQD 58
DB 1 MPGGLLLGDVAPNFEANTT-VGRIRHDFLGDWGLFSDHPNDFTPVCTTELGRAAKLAP 59
QY 59 SFTKKNCKLVGFSNDLQSHREWAKDIMAY--AGRSNLPFPLVCDPNRELAASLGIMDP 116
DB 60 EFAKRNKVLIALSIDSVEDHLAWSKDINAYNCEPTEKLPFPFIIDRRNELAILLGLMDP 119
QY 117 AEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFABILRVLSLQLTAKFPVATPV 176
DB 120 AEKDEKGMPTARVVFVFGDKKLKLSILYPATTGRNFDLIRVWISLQLTAEKRVATPV 179
QY 177 DWTAGAKCCVVPNLAEEAQRLLPKGHEALQLPSPGKPYRLRTPDP 221
DB 180 DWKDGDSVMVLPITPEEAKKLFPKGVFTKELPSGKKLYRLTPQP 224
RESULT 16
ADO24813
ID ADO24813 standard; protein; 224 AA.

XX ADO24813;
AC
XX 12-AUG-2004 (first entry)
DT
XX Human peroxiredoxin IV protein.
DE
XX
XX vulnery; anti-oxidant; free radical; peroxiredoxin; dihydrolipoic acid;
KW radiation burns; thermal burns; chemical burns; enzyme.
XX
XX Homo sapiens.
OS
XX WO2004043485-A1.
PN
XX 27-MAY-2004.
PD
XX
XX 05-NOV-2003; 2003WO-RU000473.
XX
XX 10-NOV-2002; 2002RU-00129774.
PR 29-JUL-2003; 2003RU-00123534.
XX
XX (ASCE=) AS RUSSIA INST CELL BIOPHYSICS.
XX
XX Fesenko EE, Novoselov VI, Yanin VA, Lipkin VM, Shuvaeva TM;
PI
XX WPI: 2004-420104/39.
DR N-P8DB; ADO24807.
XX
XX Composition for the antioxidant protection of cells, tissues and whole
PT organisms comprises a peroxiredoxin polypeptide, a peroxiredoxin fragment
PT and/or dihydrolipoic acid.
XX
XX Claim 8; SEQ ID NO 1; 62pp; Russian.
XX
XX The invention relates to a pharmaceutical composition for the antioxidant
CC protection of cells, tissues and whole organisms against hyperproduction
CC of free radicals comprising a peroxiredoxin polypeptide, a peroxiredoxin
CC fragment and/or dihydrolipoic acid in a total amount of 10-90 wt.%. The
CC composition is useful for treating disorders caused by an imbalance
CC between oxidative and reductive processes in mammalian organisms and
CC cells, e.g. to treat the effects of radiation, thermal and chemical burns
CC and injuries caused by disasters and fires. This sequence corresponds to
CC the human peroxiredoxin IV protein.
XX
XX Sequence 224 AA;
Query Match 53.5%; Score 638.5; DB 8; Length 224;
Best Local Similarity 56.4%; Pred. No. 4.1e-63;
Matches 127; Conservative 28; Mismatches 65; Indels 5; Gaps 3;
QY 1 MP--LNLGDSFPDFOAEALGAHFRHLHYLGDSWGMFSDHPNDFTPVCTTELAEAVKLQD 58
DB 1 MPGGLLLGDVAPNFEANTT-VGRIRHDFLGDWGLFSDHPNDFTPVCTTELGRAAKLAP 59
QY 59 SFTKKNCKLVGFSNDLQSHREWAKDIMAY--AGRSNLPFPLVCDPNRELAASLGIMDP 116
DB 60 EFAKRNKVLIALSIDSVEDHLAWSKDINAYNCEPTEKLPFPFIIDRRNELAILLGLMDP 119
QY 117 AEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFABILRVLSLQLTAKFPVATPV 176
DB 120 AEKDEKGMPTARVVFVFGDKKLKLSILYPATTGRNFDLIRVWISLQLTAEKRVATPV 179
QY 177 DWTAGAKCCVVPNLAEEAQRLLPKGHEALQLPSPGKPYRLRTPDP 221
DB 180 DWKDGDSVMVLPITPEEAKKLFPKGVFTKELPSGKKLYRLTPQP 224
RESULT 17
ABM80206
ID ABM80206 standard; protein; 224 AA.
XX
XX ABM80206;
XX

PT New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
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CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 223 AA;

Query Match 53.4%; Score 637.5; DB 7; Length 223;
Best Local Similarity 56.6%; Pred. No. 5.3e-63;
Matches 125; Conservative 28; Mismatches 65; Indels 3; Gaps 2;
QY 3 LNLGDSFPDQAEALGAHEHRLHYLGDGSGVMFNSHPNDFTPVCTTLEAAVQLQDSFTK 62
DB 4 LLLGDVAPNFEANTT-VGRIRFHDFLGDSWGLFHSHPDRDFTPVCTTLEAAVQLQDSFTK 62
QY 63 KCKLGVFSCNDLQSHREWAKDIMAY--AGRSNGLPPLVCDPNRELAASLGIMDPAEKD 120
DB 63 RNKVLIALSIDSVEDHLAWSKDINAYNCEBTEKLPFPPIIDDRNRELAALLGMLDPAEKD 122
QY 121 KKGPLTCTRCVFFISPEKKLAASILYPATTGRNFABILRVLDLSQLTAKFPVATPDVWTA 180
DB 123 EKGMPVTARVVFVFGDPDKLKLSILYPATTGRNFDEILRVVISQLTAKRKRATPDVWTKD 182
QY 181 GAKCCVVPNLAAEEAQRLLPKGHEALQLPSGKPYRLTDPD 221
DB 183 GDSVMVLPTIPEEAKKLPFGVFTKELPSGKKYLYRTPOP 223

RESULT 23
ADD48550
ID ADD48550 standard; protein; 223 AA.

XX ADD48550;
XX
DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX Human Protein P30041, SEQ ID NO 14254.
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX Homo sapiens.
OS Unidentified.

XX WO2003016475-A2.
XX
XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX (GEHO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX GENBANK; P30041.

XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.

XX Example 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC polynucleotide, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 223 AA;

Query Match 53.4%; Score 637.5; DB 7; Length 223;
Best Local Similarity 56.6%; Pred. No. 5.3e-63;
Matches 125; Conservative 28; Mismatches 65; Indels 3; Gaps 2;
QY 3 LNLGDSFPDQAEALGAHEHRLHYLGDGSGVMFNSHPNDFTPVCTTLEAAVQLQDSFTK 62
DB 4 LLLGDVAPNFEANTT-VGRIRFHDFLGDSWGLFHSHPDRDFTPVCTTLEAAVQLQDSFTK 62
QY 63 KCKLGVFSCNDLQSHREWAKDIMAY--AGRSNGLPPLVCDPNRELAASLGIMDPAEKD 120
DB 63 RNKVLIALSIDSVEDHLAWSKDINAYNCEBTEKLPFPPIIDDRNRELAALLGMLDPAEKD 122
QY 121 KKGPLTCTRCVFFISPEKKLAASILYPATTGRNFABILRVLDLSQLTAKFPVATPDVWTA 180
DB 123 EKGMPVTARVVFVFGDPDKLKLSILYPATTGRNFDEILRVVISQLTAKRKRATPDVWTKD 182
QY 181 GAKCCVVPNLAAEEAQRLLPKGHEALQLPSGKPYRLTDPD 221
DB 183 GDSVMVLPTIPEEAKKLPFGVFTKELPSGKKYLYRTPOP 223

RESULT 24
ID AAY97763
AC AAY97763 standard; protein; 221 AA.
XX
AC AAY97763;
XX
DT 06-AUG-2001 (first entry)
XX
DE I. scapularis Salp25C protein sequence.
XX
KW Salp; tick; antibody; tick immunity; infection; tick-borne disease;
KW coagulation factor Xa inhibitor; inflammatory response.
XX
OS Ixodes scapularis.
XX
PN WO20010469-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US032765.
XX
PR 03-DEC-1999; 99US-0169048P.
PR 16-OCT-2000; 2000US-0240716P.
XX
PA (UYAA) UNIV YALE.
XX
PI Kantor FS, Fikrig E, Das S;
XX
DR WPI; 2001-367810/38.
DR N-PSDB; AAA91494.
XX
PT Novel Ixodes scapularis polypeptides for conferring tick immunity and for
PT preventing the transmission of tick-borne pathogens.
XX
PS Claim 20; Fig 2; 137pp; English.
XX
CC This sequence is an Ixodes scapularis polypeptide of the invention. The
CC proteins of the invention are 15 tick Salp proteins. The proteins,
CC antibodies against them or pharmaceutical composition comprising a fusion
CC protein or a multimeric protein and at least one additional non-Ixodes
CC scapularis polypeptide, can be administered to a subject to confer tick
CC immunity and therefore prevent infection by a tick-borne disease.
CC Inhibiting coagulation factor Xa activity comprises administering to a
CC subject a polypeptide selected from Salp14A, Salp9A or a fragment of
CC these having Xa inhibiting activity, inhibiting histamine activity
CC comprises administering a Salp25D polypeptide or its histamine binding
CC fragment to a subject, and inhibiting or preventing an inflammatory
CC response comprises administering a polypeptide selected from a Salp15,
CC Salp25C, Salp13 or a fragment of these having the same activity. The
CC protein or its immunogenic fragment may be used to produce monoclonal
CC antibodies that are screened for their ability to confer tick immunity
CC when used to immunise naive animals. The antibody can be used to screen
CC for expression of I. scapularis polypeptides, either in libraries
CC constructed from I. scapularis nucleic acid molecules or from other
CC samples in which proteins may be present, and for purifying or removing
CC polypeptides from a given sample to block or bind to specific epitopes on
CC the polypeptides and to direct various molecules, such as toxins, to
CC ticks
XX
SQ Sequence 221 AA;

Query Match 51.8%; Score 619; DB 4; Length 221;
Best Local Similarity 51.8%; Pred. No. 6.4e-61;
Matches 114; Conservative 35; Mismatches 69; Indels 2; Gaps 2;

QY 2 PLNLGSDPDPQAEALCAEHLRLHEYLGDWGMVFSHPNDFTPVCTTELAAVAKLQDSFT 61
DB 3 PLNLGDPFPNFTCDTTEGK-IDFHEWLGNSWGLFSGHPADYTPVCTSELARAAQLHHVFQ 61
QY 62 KKNCKLVGFCNDLQSHREKAWDKIMAYAG-RSGNLPFLVCDPNRELAASLGIMDPAEKD 120

DB 62 KKGVKLIALLSCDSVESHRCWIKDINAFGELPGPPYPPIADEKRDIAVKLGMLDPVEKD 121
QY 121 KKGPLPTCRCVFFISPEKKLAASILYPATGTGRNFAEILRLVLSLQLTAKFPVATPVDWTA 180
DB 122 KEGPLPTCRVFIIGFDKMKLSMLYPATGTGRNFDVLRATDSLLVTETRKVATPAGWQK 181
QY 181 GAKCCVVPNLAAEEAQRLLPKGHEALQLPSGPKYLRLTPD 220
DB 182 GTPCMVLPSTVEEILKLPFTGIKQYEVSPGKNYLRRTTMD 221

RESULT 25
AAW88273
ID AAW88273 standard; protein; 235 AA.
XX
AC AAW88273;
XX
DT 29-MAR-1999 (first entry)
XX
DE Dirofilaria immitis thioredoxin peroxidase PDITPx2(235).
XX
KW Thioredoxin peroxidase type-2; TPx-2; PDITPx2(235); vaccine;
KW anthelmintic; helminth; heartworm disease; elephantiastis; hydrocele;
KW therapy; diagnosis.
XX
OS Dirofilaria immitis.
XX
FH Key Location/Qualifiers
FT Active-site 49
XX
PN WO9852971-A1.
XX
PD 26-NOV-1998.
XX
PF 21-MAY-1998; 98WO-US010474.
XX
PR 23-MAY-1997; 97US-00862540.
XX
PA (HESK-) HESKA CORP.
PA (COLS) UNIV COLORADO STATE RES FOUND.
XX
PI Chandrashekar R, Tsuji N;
XX
XX WPI; 1999-070138/06.
DR N-PSDB; AAW84203, AAW84206, AAW84208.
XX
PT New isolated thioredoxin peroxidase type-2 nucleic acid - obtained from a
PT Dirofilaria and Brugia, used to develop products for protection against
PT parasite helminth disease such as heartworm disease.
XX
PS Claim 10; Page 58-59; 79pp; English.
XX
CC This polypeptide, designated PDITPx2(823), comprises the thioredoxin
CC peroxidase type-2 (TPx-2) of Dirofilaria immitis. A cDNA clone (see
CC AAW84203) encoding the polypeptide was isolated from a D. immitis L4 cDNA
CC library on the basis of its ability to encode a protein that selectively
CC bound at least one component of immune serum from a rabbit immunised with
CC a peptide derived from a Brugia malayi transmembrane protein. The deduced
CC polypeptide shows homology to Onchocerca volvulus adult TPx protein. D.
CC immitis and B. malayi TPx-2 nucleic acid sequences (see AAW84203-14) and
CC polypeptides (see AAW88273-74) are used in vaccines (including genetic
CC vaccines, recombinant virus vaccines and recombinant cell vaccines) for
CC the protection of animals against parasite helminth disease, especially
CC heartworm disease, elephantiastis and hydrocele (claimed). They can also
CC be used for detection, diagnosis and drug screening
XX
SQ Sequence 235 AA;

Query Match 51.8%; Score 618.5; DB 2; Length 235;
Best Local Similarity 54.1%; Pred. No. 8e-61;
Matches 124; Conservative 28; Mismatches 66; Indels 11; Gaps 3;

QY 5 LGDSFPDFQAEALGAEHLRLHEYLGDWGMVFSHPNDFTPVCTTELAAVAKLQDSFTK 63

Db 7 LGDKFPDFRAETWEGFTIPSFYDWIGKDSWAILFESHPRDFTPVCTTTELARLVOLAPBPKR 66
QY 64 NCKLVGSCNDLQSHREWAKIMAYAGR-----SGN-LPPELVCDNRELAASLGI 113
Db 67 NVKLGISCSASHSRKRWDIDIAVCOKKNDGDTCCSGNKLPFPIIADENRELTGLM 126
QY 114 MDPAEKKGLPLTRCVRFFISPEKLAASILYPATTGRNFAELRLVLDLSQLTAKPPVA 173
Db 127 MDPDERDENGALTARCVFIIGPEKTLKLSILYPATTGRNFDLRLVVDLSQLTAVKVA 186
QY 174 TPVDWTAGAKCCVVPNUAAEQRLLPKGHEALQLPSGKPYRLRLTPDDR 222
Db 187 TPVDWKGDDCVVLPTDIDTTEAKKLFGEKINTIELPSGKHYLRMVAHPK 235
RESULT 26
AAG66167
ID AAG66167 standard; protein; 222 AA.
XX AAG66167;
AC
XX
DT 17-JUN-2002 (first entry)
XX
DE Tick peroxidoxin (Prx) protein.
XX
XX Peroxiredoxin; Prx; tick; vaccine; antitick agent.
XX
XX Haemaphysalis longicornis.
OS
XX JP2002010785-A.
PN
XX
XX 15-JAN-2002.
XX
XX 29-JUN-2000; 2000JP-00196620.
PF
XX 29-JUN-2000; 2000JP-00196620.
PR
XX (FARB) BAYER KK.
PA
XX
XX WPI; 2002-298337/34.
DR
XX N-PSDB; ABL40531.
XX
XX Tick peroxidoxin, a nucleic acid molecule encoding it and its use.
XX
XX Claim 2; Page 7; 10pp; Japanese.
XX
CC The invention provides a gene encoding Haemaphysalis longicornis
CC peroxidoxin (Prx). The Prx protein can be expressed by standard
CC recombinant methodology. The tick Prx protein and the nucleic acid can be
CC used for a new target of tick vaccine and antitick agent. The present
CC sequence represents the tick Prx protein
XX
SQ Sequence 222 AA;
Query Match 51.0%; Score 609.5; DB 5; Length 222;
Best Local Similarity 52.3%; Pred. No. 7.6e-60;
Matches 116; Conservative 32; Mismatches 69; Indels 5; Gaps 4;
QY 2 PLNLGDPFPDFOAE-ALGAEBHRLHLEYLGDGWSGVMFSPHNDP-TPVCTTELAAVAKLQDS 59
Db 3 PLNLGDPFPNFTCETTGTIDF--HQWLGDGSGILFESHDPADYTPVCTTELAAVAKLQAHV 60
QY 60 FTKKNCVLGVSCNDLQSHREWAKIMAYAG-RSGNLPFLVCDPNRELAASLGIWDPAE 118
Db 61 FAQKGVKIIALSCDSVDSHGWTKDTEAFGELPDGPPFPYPIIADEKREIAVKLGLMDPVE 120
QY 119 KDKKGLPLTRCVRFFISPEKLAASILYPATTGRNFAELRLVLDLSQLTAKPPVATPVDW 178
Db 121 KDEGLPLTRCVRFFISPEKLAASILYPATTGRNFAELRLVLDLSQLTAKPPVATPAGW 180
QY 179 TAGAKCCVVPNUAAEQRLLPKGHEALQLPSGKPYRLRLTPD 220

Db 181 KKGTPCMVLPSVTEBIPKLPFTGIKQYDVPSGKYLRTMD 222
RESULT 27
ABU07560
ID ABU07560 standard; protein; 224 AA.
XX
AC ABU07560;
XX
DT 18-MAR-2003 (first entry)
XX
DE Mouse antioxidant protein 2 related sequence 1.
XX
XX Mouse; antioxidant protein 2; Aop2; atherosclerosis; antiatherosclerotic;
KW antioxidant; atherosclerotic lesion; oxidative damage; heart surgery;
KW Aop2-rs1.
XX
XX Mus sp.
OS
XX US2002142417-A1.
PN
XX 03-OCT-2002.
PD
XX 28-MAR-2001; 2001US-00819505.
PF
XX 02-APR-1997; 97US-0040898P.
PR
XX 01-APR-1998; 98US-00053088.
XX
XX (PAIG/) PAIGEN B.
PA (BEIE/) BEIER D R.
XX
XX Paigen B, Beier DR;
PI
XX WPI; 2003-155944/15.
DR N-PSDB; ABX15216.
XX
XX Novel antioxidant protein-2 polypeptide useful for diagnosing
PT predisposition to atherosclerotic lesions in subject, and screening a
PT compound for the protein stimulatory activity.
XX
PS Example 8; Fig 8B; 54pp; English.
XX
CC The invention relates to an isolated antioxidant protein-2 polypeptide,
CC designated Aop2, its antigenic fragment or the nucleotide encoding Aop2
CC (Aop2 NA). Also included are Aop2 NA oligonucleotides, screening a
CC compound for Aop2 stimulatory activity, screening a compound for anti-
CC atherosclerotic activity (by providing a lipid, contacting the lipid with
CC a candidate antioxidant, and determining the oxidation state of the
CC lipid), an anti-Aop2 mono/polyclonal antibody, an Aop2 NA expression
CC vector, a host cell comprising Aop2 NA and reducing atherosclerotic
CC lesions in a subject (by administering a lipid antioxidant composition to
CC the subject). Aop2 is useful for diagnosing a predisposition to
CC atherosclerotic lesions in a subject involving determining the
CC antioxidant activity of an Aop2 polypeptide of the sample, or the level
CC of an Aop2 polypeptide in cells of the sample or involves polymerase
CC chain reaction (PCR), and the determining step is performed by contacting
CC the sample with an anti-Aop2 antibody, or determining the sequence of
CC nucleic acid from the sample that encodes an Aop2 polypeptide. Aop2 is
CC also useful for screening a compound for Aop2 stimulatory activity. Aop2
CC NA is useful for increasing Aop2 function in a cell. The expression
CC vector may be a viral vector, encapsulated in a liposome. The viral
CC vector is adenoviral, retroviral, vaccinia, adeno-associated viral
CC vector, or herpes viral vector. The cell is located in a human subject,
CC or an experimental animal. The promoter is cytomegalovirus (CMV), rous
CC sarcoma virus (RSV), or E1A. Aop2 is also useful in preventing oxidative
CC damage in vivo, for e.g., during heart surgery, where blood is oxygenated
CC outside the body. Aop2 or Aop2 NA is useful for treating atherosclerosis.
CC The present sequence represents mouse Aop2-rs1, Aop2 related sequence 1
XX
SQ Sequence 224 AA;
Query Match 50.9%; Score 607.5; DB 6; Length 224;
Best Local Similarity 52.7%; Pred. No. 1.3e-59;

Matches 119; Conservative 32; Mismatches 68; Indels 7; Gaps 4;

QY 1 MP--LNLGDSFPDQAE-ALGAEHFLRHLHEYLGDGSGWFMFHPNDFTPVCTTTELAEAVKLQ 57
 DB 1 MPGLLGEAPDFEANTTIG--RIRFHDPLGNSGMLFSPKDFTPVCTTTELGRAAKLA 58
 QY 58 DSFTKKNCKLVGSCNDLQSHREWAKDIMAYAGRS--GNLPEPLVCDPNRELAASLGIMD 115
 DB 59 PEFKRNKVLIALUSVDSVDHLAWSKDINAYGATPKELPFPIIDDKORDISILFCMLD 118
 QY 116 PAEKDKKGLPLTCRCVFFTSPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATP 175
 DB 119 PVEKDANSPLTARGVIFGPDKKLWMLLYPNSTGRNFEILRVLDLSQLTETKVPATP 178
 QY 176 VDMTAGAKCCVNPVLAABEAQRLLPKGHEALQLPSGKPYRLRTPDP 221
 DB 179 VDMKGESVMVLPDPEEAKRCPKPGIGSTTKLPKSGKNVLRYPQP 224

RESULT 28

ABB59626
 ID ABB59626 standard; protein; 222 AA.

XX AC ABB59626;

DT 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 5670.

XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.

OS Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

PR 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

DR N-PSDB; ABL03729.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.

XX Disclosure; SEQ ID NO 5670; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL10511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 222 AA;

Query Match 49.2%; Score 588; DB 4; Length 222;
 Best Local Similarity 49.3%; Pred. No. 2e-57;
 Matches 108; Conservative 38; Mismatches 71; Indels 2; Gaps 2;

QY 3 LNLGDSFPDQAEALGAEHFLRHLHEYLGDGSGWFMFHPNDFTPVCTTTELAEAVKLQDSFTK 62
 DB 6 LNLGDSFPDQAEALGAEHFLRHLHEYLGDGSGWFMFHPNDFTPVCTTTELAEAVKLQDSFTK 64
 QY 63 KCKLVGSCNDLQSHREWAKDIMAYAGRSGNLPPPLVCDPNRELAASLGIMDPAEKOKK 122
 DB 65 RGVKPIALSCTVESHKGWIEDIKSF-GKLSSTDFPIADKKELAKENMLDKOBINAE 123
 QY 123 GLPLTCRCVFFTSPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPVDMWTAGA 182
 DB 124 GIPLTCRAVVFVDDKKLRLSLILYPATTGRNFEILRVLDLSQLTQTKSVATPADWKQGG 183
 QY 183 KCCVNPVLAABEAQRLLPKGHEALQLPSGKPYRLRTPDP 221
 DB 184 KCVLFTVKAEDVPKLPDPDGIETIELPSGKSYLRITPQP 222

RESULT 29

AAR34196

ID AAR34196 standard; protein; 250 AA.

XX AC AAR34196;

DT 25-MAR-2003 (revised)

DT 04-AUG-1993 (first entry)

XX O-CSF.

XX Osteoclast colony stimulating factor; O-CSF; hypercalcaemia; inducing;
 KW murine; mammary; tumour; tetracycline-resistant acid phosphatase; TRAP;
 KW progenitor; bone marrow; SDS-PAGE.

OS Mus musculus.

XX WO9307271-A1.

XX 15-APR-1993.

XX 30-SEP-1992; 92WO-US008322.

XX 01-OCT-1991; 91US-00770042.

XX (WASH-) WASHINGTON RES FOUND.

XX Lee MY, Osborne WRA, Byre DR;

XX WPI; 1993-134460/16.

DR N-PSDB; AAQ38837.

XX New osteoclast colony stimulating factor - induces osteoclast
 PT progenitor(s) for differentiation and proliferation from bone marrow for
 PT treatment of eg. osteopetrosis.

XX Claim 13; Fig 15; 59pp; English.

XX This sequence represents osteoclast colony stimulating factor (O-CSF)
 CC which was isolated from conditioned medium of a hypercalcaemia-inducing
 CC murine mammary tumour. O-CSF protein is capable of stimulating growth of
 CC tetracycline-resistant acid phosphatase (TRAP)-positive osteoclast progenitors
 CC in bone marrow cell cultures. O-CSF has an apparent molecular weight of
 CC approx. 15-25 kD, with a peak of biological activity at approx. 20 kD, as
 CC determined by SDS-PAGE and biological assay. The O-CSF protein may be
 CC purified from the culture medium of CESJ-3 cells and has an osteoclast
 CC progenitor stimulating activity of at least 660,000 U/mg. (Updated on 25-
 CC MAR-2003 to correct PN field.)

XX SQ Sequence 250 AA;

Query Match 49.0%; Score 585; DB 2; Length 250;
 Best Local Similarity 53.5%; Pred. No. 5.3e-57;
 Matches 116; Conservative 29; Mismatches 64; Indels 8; Gaps 4;

QY 6 GDSFPDQAE-ALGAEHFLRHLHEYLGDGSGWFMFHPNDFTPVCTTTELAEAVKLQDSFTKKN 64

Db 1 GDEAPNEANTTIG--RIRFHDPLGDSWGLFSPDRDFTPVCTTELGRAAKLAPEFAKRN 58
QY 65 CKLVGFSNDLQSHREWAKDIMAYGR--SCNLPPLVCDPNRELAASLGTMDBAEKDKK 122
Db 59 VKLTALSIDSVEDHLAWSKDINAYNGETPEKLPFPFIIDDKGRDLAILGLMLDDEVQKDN 118
QY 123 GLPLTCTRCVFFISPEKKLAASILYPATTGRNFABILRVLSLQLTAKFPVPVDTWDTAGA 182
Db 119 NMPVTARVVFIFGDPDKLKLILYPATTGRNFDEILRVLSLQLTGTPKVPATPVVDVKGE 178
QY 183 KCCVVPNLAABEAQRLLPKGHEALQLPSGKPYLRLTP 219
Db 179 SVMVVPITLSEBAKQCFKPGVFTKELPSGK---KLPP 212

RESULT 30
ADO24814
ID ADO24814 standard; protein; 177 AA.
XX
AC ADO24814;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human peroxiredoxin IV protein N-terminal fragment.
XX
KW vulnery; anti-oxidant; free radical; peroxiredoxin; dihydroliipoic acid;
KW radiation burns; thermal burns; chemical burns; enzyme.
XX
OS Homo sapiens.
XX
PN WO2004043485-A1.
XX
PD 27-MAY-2004.
XX
PF 05-NOV-2003; 2003WO-RU000473.
XX
PR 10-NOV-2002; 2002RU-00129774.
PR 29-JUL-2003; 2003RU-00123534.
XX
PA (ASCE=) AS RUSSIA INST CELL BIOPHYSICS.
XX
PI Feenko EE, Novoselov VI, Yanin VA, Lipkin VM, Shuvaeva TM;
XX
DR WPI; 2004-420104/39.
DR N-PSDB; ADO24808.
XX

Composition for the antioxidant protection of cells, tissues and whole
organisms comprises a peroxiredoxin polypeptide, a peroxylredoxin fragment
and/or dihydroliipoic acid.
XX
PS Claim 8; SEQ ID NO 2; 62pp; Russian.
XX
CC The invention relates to a pharmaceutical composition for the antioxidant
protection of cells, tissues and whole organisms against hyperproduction
of free radicals comprising a peroxiredoxin polypeptide, a peroxylredoxin
fragment and/or dihydroliipoic acid in a total amount of 10-90 wt.%. The
composition is useful for treating disorders caused by an imbalance
CC between oxidative and reductive processes in mammalian organisms and
cells, e.g. to treat the effects of radiation, thermal and chemical burns
CC and injuries caused by disasters and fires. This sequence corresponds to
CC the N-terminal fragment of the human peroxiredoxin IV protein.
XX
SQ Sequence 177 AA;

Query Match 42.5%; Score 507.5; DB 8; Length 177;
Best Local Similarity 57.3%; Pred. No. 1.8e-46;
Matches 102; Conservative 23; Mismatches 48; Indels 5; Gaps 3;

QY 1 MP--LNLGDSFPDQAEALGAHFRRLHEYLIGDSWGVMSHPNDPTPVCTTELEAVKLQD 58
Db 1 MPGLLLGDVAPNPEANTT-VGRIRFDLGLDSWGLFSPDRDFTPVCTTELGRAAKLAP 59

QY 59 SFTKXCKLVGFSNDLQSHREWAKDIMAY--AGRSNLPPLVCDPNRELAASLGIMDP 116
Db 60 EFAKRNVKLTALSIDSVEDHLAWSKDINAYNCEPTEKLPFIIDDRNRELAAILGLMLDP 119
QY 117 AEKDKKGLPLTCTRCVFFISPEKKLAASILYPATTGRNFABILRVLSLQLTAKFPVPVAT 174
Db 120 AEKDEKGMPTARVVFVFGDPDKLKLILYPATTGRNFDBILRVVLSLQLTAEKRVAT 177
RESULT 31
ADS24874
ID ADS24874 standard; protein; 212 AA.
XX
AC ADS24874;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #13907.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
DR WPI; 2004-061375/06.
XX

New recombinant DNA construct comprising a promoter positioned to provide
for expression of a polynucleotide encoding a polypeptide from a
microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 13907; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
promoter functional in a plant cell, where the promoter is positioned to
provide for expression of a polynucleotide encoding a polypeptide from a
microbial source. The invention also relates to a transformed plant
comprising the recombinant DNA construct and a method of producing a
transformed plant having an improved property. The plant is a crop plant
such as maize or soybean. The method of producing a transformed plant
having an improved property comprises transforming a plant with the
recombinant DNA construct and growing the transformed plant, where the
polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
content, improved yield by modification of carbohydrate, nitrogen or
phosphorus use and/or uptake, by modification of photosynthesis or by
providing improved plant growth and development under at least one stress
condition, improved lignin production or improved galactomannan

CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 212 AA;

Query Match 42.5%; Score 507.5; DB 8; Length 212;
Best Local Similarity 47.3%; Pred. No. 2.3e-48;
Matches 105; Conservative 34; Mismatches 70; Indels 13; Gaps 5;
QY 1 MPLNLGDSFPDFOAEALGAEHRLHEVLGDSWGMFSPNDFTPVCTTTELAEAVKLQDSF 60
Db 1 MSRLGDIADFPQDS-SAGKIRFHEWLGSWGLFSPADFTPVCTTTELGTAKURDEF 59
QY 61 TKKNCKLVGFCNDLQSHREWAKDIMAYAGRSNGLPPLVCDPNRELAASLGIMDPAEKD 120
Db 60 TKRGVKAIALSVDPVDSHHKWIEDINETQNTIVN--FPILADADRVSDLYLIHFNAND 117
QY 121 KGLPLTCRCVFFISPEKKLAASILYPATTGRNFAELRLVLDLSQLTAKFPVATPVVDWTA 180
Db 118 ----TLTVRSLFVIDENKKRLITYTPASTGRNFHEILRLVIDLSQLTDNYKVATPANWQD 173
QY 181 GAKCCVVPNLAAE-EAQRLLPKGHEALQLPSGPKPYLRLTPDP 221
Db 174 GEEVIVPSLKDEDEIKQRFPGTRAV-----KPYLRLTPQP 210

RESULT 32
ABB65897
ID ABB65897 standard; protein; 220 AA.
AC ABB65897;
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 24483.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
XX
XX 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX
XX N-PSDB; ABL10000.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.
XX
XX Disclosure; SEQ ID NO 24483; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX ABB72072). The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 220 AA;
Query Match 42.0%; Score 501.5; DB 4; Length 220;
Best Local Similarity 44.5%; Pred. No. 1.2e-47;
Matches 97; Conservative 39; Mismatches 79; Indels 3; Gaps 3;
QY 3 LNLGDSFPDFOAEALGAEHRLHEVLGDSWGMFSPNDFTPVCTTTELAEAVKLQDSFTK 62
Db 1 MRLGQTVNFEADTTKGP-IKFHEMQGNSVVLFSPADFTPVCTTTELGRIVHQPEFAK 59
QY 63 KNCKLVGFCNDLQSHREWAKDIMAYA-GRSNGLPPLVCDPNRELAASLGIMDPAEKOK 121
Db 60 RNTKCLAHSDALNSHVDWVNDIKSYCLDIPGDFPYPIIADPTDRLAVSLGLMDERQKKD 119
QY 122 KGLPLTCRCVFFISPEKKLAASILYPATTGRNFAELRLVLDLSQLTAKFP-VATPVVDWTA 180
Db 120 PEVGKTIKRALFTISPDHKVRLSMFYPMSTGRNVDEILRTIDSLSQLTDLRLKVVATPANWTP 179
QY 181 GAKCCVVPNLAAEAEQRLLPKGHEALQLPSGPKPYLRLT 218
Db 180 GTKWMLPTVTDDEAHKLFPGKGVKMPFSGVNYVRTT 217
RESULT 33
ABB59059
ID ABB59059 standard; protein; 220 AA.
XX
XX ABB59059;
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 3969.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX
XX pharmaceutical.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
XX
XX 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX
XX N-PSDB; ABL03162.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.
XX
XX Disclosure; SEQ ID NO 3969; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences

[illegible]

RESULT 34	
ABO68070	
ID	ABO68070 standard; protein; 222 AA.
XX	
AC	ABO68070;
XX	
DT	29-JUL-2004 (first entry)
XX	
DE	Pseudomonas aeruginosa polypeptide #245.
XX	
KW	Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX	
OS	Pseudomonas aeruginosa.
XX	
PN	US6551795-B1.
XX	
PD	22-APR-2003.
XX	
PF	18-FEB-1999; 99US-00252991.
XX	
PR	18-FEB-1998; 98US-0074788P.
XX	
PA	27-JUL-1998; 98US-0094190P.
XX	
XX	(GENO-) GENOME THERAPEUTICS CORP.
XX	
PI	Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX	
DR	WPI; 2003-615309/58.
XX	
DR	N-PSDB; ABD01641.
XX	

Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection

PS Disclosure; SEQ ID NO 16816; 455pp; English;

The invention relates to *Pseudomonas aeruginosa* polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a *P. aeruginosa* nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-*P. aeruginosa* drugs, as templates for recombinant production of *P. aeruginosa*-derived peptides or polypeptides, as target components for diagnosis and/or treatment of *P. aeruginosa*-caused infection, and in detection of *P. aeruginosa* sequences or other sequences of *Pseudomonas* species using biochip technology. Sequences AB067826-AB084396 represent *P. aeruginosa* polypeptides of the invention. Note: The

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CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 222 AA;

Query Match 41.7%; Score 497.5; DB 7; Length 222;
Best Local Similarity 46.8%; Pred. No. 3.3e-47;
Matches 104; Conservative 34; Mismatches 71; Indels 13; Gaps 5

QY 1 MPLNLGDSFPDFOAEALGAHFRLHVEYLGDSWGVMFSPHPNDFTPVCTTELAENVKLQDSF 60
DB 11 MSLELGDIAPIPDFFQDS--SEGRIRLHLEWLGDSWGLFSPADFTPVCTTELGFTAKLKQDF 69
QY 61 TKKNCKLVGFSNDLQSHREWAKDIMAYAGRSGNLPPPLVCDPNRELAASLGIMPAEKD 120
DB 70 AQGVKVLVSVPVESHKLWIDINTQDTRVN--FPITADARKVSELVDLIHPNAND 127
QY 121 KXGLPLTCRCVFFISPEPKLAASILYIPATTGRNFAEILRLVLDLSQLTAKFPVPVDWTA 180
DB 128 ----TLTVRSLSFIIDPNKKVRLIITYPASTGRNFNEILRLVIDLSQLTDEHKVATPANWD 183
QY 181 GAKCCVVPNLA--AEEAQRLLPKGHEALQLPSGKPYLRLTPDP 221
DB 184 GDEWTVPSLKDSEEEKRRFPKGVRAV-----KPYLRLTPDP 220

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RESULT 35

ABB80958
ID ABB80958 standard; protein; 218 AA.

AC ABB80958;

21-OCT-2002 (first entry)

DE Barley 1-Cys peroxiredoxin (HvPer1).

Oil palm; embryogenic-specific polypeptide; plant; OPEml; apoptosis;
 KW embryogenesis; molecular marker; antioxidant; antiaging; peroxiredoxin;
 KW barley; l-Cys peroxiredoxin; HvPer1.

XX
OS
Hordeum vulgare.

XX PN EP1217068-A2

XX
PD 26-JUN-2002

XX
DE
20-DEC-2001. 2001EB-0031070E

XX
PB 20-DEC-2000. 2000AII-00002213

XX
DA
(MAD) 1 MAY 1978
DAYM
OTY
DOR

XX
BT
XX

XX
NDT : 0000 EF0105 / F0

XX Novel isolated embryogenic-specific polypeptide from oil-palm, OPEm1, and
PT polynucleotides encoding them, useful as molecular markers for plant
PT embryogenesis and for inhibiting/retarding apoptosis in plant, animal
PT cells.

PS Disclosure: Fig 6. 41pp. English

The invention relates to isolated embryonic-specific polypeptide from oil palm, OPem1 and encoding polynucleotides. OPem1 is present in plant zygotic embryos or embryogenic callus and not present in non-embryogenic tissue. OPem1 can be expressed by standard recombinant technology. The OPem1 polypeptide is useful for modulating apoptotic processes in a cell. The encoding polynucleotide is useful for detecting embryogenic plant material. The OPem1 polypeptide and polynucleotides act as molecular markers for a plant physiological process, specifically plant embryogenesis. The molecular markers enable embryogenic tissue to be

CC detected in vitro. They are also useful for inhibiting or retarding
 CC apoptotic processes in both plant and animal cells. OPEm1 has antioxidant
 CC activity, and thus is useful in tablet or cream as an antiaging agent.
 CC OPEm1 encodes a peroxiredoxin useful for the modulation of cellular
 CC apoptotic processes and is useful as an immunological agent to generate
 CC antibodies useful as diagnostic markers. The present sequence represents
 CC a barley 1-Cys peroxiredoxin (HvPer1) used in comparison studies with the
 CC oil palm OPEm1 polypeptide
 XX
 SQ Sequence 218 AA;

Query Match 41.5%; Score 495; DB 5; Length 218;
 Best Local Similarity 43.4%; Pred. No. 6.2e-47;
 Matches 95; Conservative 43; Mismatches 77; Indels 4; Gaps 4;
 QY 1 MP-LNLGDSPPDQAEALGAHEHRLHEYLGDSDGVGMFSPNDFTPVCTTELAABAVKLQDS 59
 DB 1 MPGLTIGDTPVNLDELSTHGK-IRIHQVGVNGYVILFSPGDFTPVCTTELAAMANYAKE 59
 QY 60 FTKKNCKLVGFSNDLQSHREWAKDIMAYAGRSNLPFPLVCDPNRELAASLGIMDPAEK 119
 DB 60 FEKRGVKLLGISDQVQSHKEWTKDIEAYKPGS-KVTYPIADPDRSAIKQLNMVDPDEK 118
 QY 120 DKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLSLQLTAKFPVATPVDMT 179
 DB 119 DAQG-QLPSTLHIVGDKVKVLSFLYPSCTGRNMDVVRVDSLLTAAKHKATPANWK 177
 QY 180 AGAKCCVVPNLAABEAAQRLLPKGHEALQLPSGKPYRLRLT 218
 DB 178 PGECWVIAPGVSDBEAKMFPQGFETADLPSSKGYLRFT 216

RESULT 36

ADN21975
 ID ADN21975 standard; protein; 212 AA.

XX AC ADN21975;

XX DT 02-DEC-2004 (first entry)

XX DE Bacterial polypeptide #4628.

XX KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.

XX OS Bacteria.

XX PN US2003233675-A1.

XX PD 18-DEC-2003.

XX PF 20-FEB-2003; 2003US-00369493.

XX PR 21-FEB-2002; 2002US-0360039P.

XX PA (CAOY/) CAO Y.

XX PA (HINK/) HINKLE G J.

XX PA (SLAT/) SLATER S C.

XX PA (CHEN/) CHEN X.

XX PA (GOLD/) GOLDMAN B S.

XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX WI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.

XX PS Claim 1; SEQ ID NO 4628; 122pp; English.
 XX CC The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 212 AA;

Query Match 41.4%; Score 494.5; DB 8; Length 212;
 Best Local Similarity 45.9%; Pred. No. 6.8e-47;
 Matches 102; Conservative 37; Mismatches 70; Indels 13; Gaps 5;

QY 1 MPLNLGDSPPDQAEALGAHEHRLHEYLGDSDGVGMFSPNDFTPVCTTELAABAVKLQDSF 60

DB 1 MSRLGLDIAPDFEQQS-SVGPTRFHEWLGDSGVLFSPADFTPVCTTELGLTAKLASEF 59

QY 61 TTKNCKLVGFSNDLQSHREWAKDIMAYAGRSNLPFPLVCDPNRELAASLGIMDPAEKD 120

DB 60 EKRNVTITALSVDSAESHKEWIKDI--NETQAAVGFPIADGDKRVSELYDMIHFNANE 117

QY 121 KKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLSLQLTAKFPVATPVDMT 180

DB 118 ----TLTVRSFLVIDPKKKVLIITYPASTGRNFDVLRVIDLSLQLTDSHVSATPGNWK 173

QY 181 GAKCCVVPNLAABE-AQRLLPKGHEALQLPSGKPYRLRLTDP 221

DB 174 GDDVWIVPSLKDDEIHKQKFPKGYKAL----RPYLRLMTQP 210

RESULT 37

ADN24733
 ID ADN24733 standard; protein; 212 AA.

XX AC ADN24733;

XX DT 02-DEC-2004 (first entry)

XX DE Bacterial polypeptide #7386.

XX KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.

XX OS Bacteria.

XX PN US2003233675-A1.

PD 18-DEC-2003.
XX
XX
XX 20-FEB-2003; 2003US-00369493.
XX
XX 21-FEB-2002; 2002US-0360039P.
XX
XX (CHAOY/) CAO Y.
XX (HINK/) HINKLE G J.
XX (SLAT/) SLATER S C.
XX (CHEN/) CHEN X.
XX (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
XX for expression of a polynucleotide encoding a polypeptide from a
XX microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 7386; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in a plant cell, where the promoter is positioned to
XX provide for expression of a polynucleotide encoding a polypeptide from a
XX microbial source. The invention also relates to a transformed plant
XX comprising the recombinant DNA construct and a method of producing a
XX transformed plant having an improved property. The plant is a crop plant
XX such as maize or soybean. The method of producing a transformed plant
XX having an improved property comprises transforming a plant with the
XX recombinant DNA construct and growing the transformed plant, where the
XX polynucleotide or polypeptide is useful for improving plants with
XX The recombinant DNA construct is useful for producing plants with
XX improved plant properties, e.g. improved cold, heat or drought tolerance,
XX tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX increased resistance to plant disease, better growth rate by modification
XX of the cell cycle pathway with plant growth regulators, increased rate of
XX homologous recombination, modified seed oil or protein yield and/or
XX content, improved yield by modification of carbohydrate, nitrogen or
XX phosphorus use and/or uptake, by modification of photosynthesis or by
XX providing improved plant growth and development under at least one stress
XX condition, improved lignin production or improved galactomannan
XX production. This sequence represents a bacterial polypeptide used in the
XX scope of the invention. Note: The sequence data for this patent did not
XX form part of the printed specification but was obtained in electronic
XX format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX SQ Sequence 212 AA;

Query Match 41.4%; Score 494.5; DB 8; Length 212;
Best Local Similarity 45.9%; Pred. No. 6.8e-47;
Matches 102; Conservative 37; Mismatches 70; Indels 13; Gaps 5;

Qy 1 MPLNLGDSFPDFOAEALGAEHFRLHLYLGDGSGVMFSDHNDFTPVCTTELAELAVKLQDSF 60
Db 1 MSLRLGDIAPDFEQQS-SVGPIRFHEWLGDGSGWGLFSDHPADFTPVCTTELGTLAKLASEF 59

Qy 61 TKKNCKLVGSCNDLQSHREWAKDIMAYAGRSNGLPPLVCDPNRELAASLGIMDPAEKD 120
Db 60 EKRNVKTIALSVDAESHKGIWKDI--NETQANVGFPILADGDKRVSELYDMMHFNANE 117

Qy 121 KKGGLPLTRCVRFFISPEKLAASILYPATTTGRNFAELRLVLDLSQLTAKFPVATPVDWTA 180
Db 118 ----TLTVRSILFVIDPKKKVRLIITYPASTGRNFDEVLRLVLDLSQLTDSHVSATPGNWKQ 173

Qy 181 GAKCCVVPNLAAEF-AORLLPKGHEALQLPSGKPYLRLTPDP 221
Db 174 GDDVIVPSLKDSEIIRKQPKGYKAL-----RPLYRLMTPOP 210

RESULT 38
ADA34041
ID ADA34041 standard; protein; 216 AA.

XX ADA34041;
XX
XX 20-NOV-2003 (first entry)
XX
XX Acinetobacter baumannii protein #1202.
XX
XX Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
XX plant biocontrol agent.
XX
XX Acinetobacter baumannii.
XX
XX US6562958-B1.
XX 13-MAY-2003.
XX
XX 04-JUN-1999; 99US-00328352.
XX
XX 09-JUN-1998; 98US-0088701P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Breton G, Bush D;
XX
XX WPI; 2003-576092/54.
XX N-PSDB; ADA29915.
XX
XX New Acinetobacter baumannii proteins and nucleic acids, useful as reagents
XX for diagnosing a bacterial disease, as components of antibacterial
XX vaccines, as targets for antibacterial drugs, to detect the presence of
XX A. baumannii and other Acinetobacter species in a sample, in screening
XX compounds for the ability to interfere with the A. baumannii life cycle
XX or to inhibit A. baumannii infection, and as biocontrol agents for
XX plants. The present sequence represents the amino acid sequence of an A.
XX baumannii protein.
XX
XX SQ Sequence 216 AA;

Query Match 41.4%; Score 494.5; DB 6; Length 216;
Best Local Similarity 45.7%; Pred. No. 7e-47;
Matches 102; Conservative 37; Mismatches 69; Indels 15; Gaps 6;

Qy 1 MPLNLGDSFPDFOAEALGAEHFRLHLYLGDGSGVMFSDHNDFTPVCTTELAELAVKLQDS 59
Db 4 MTLRLGDTAPDFQESSEGTINF--YDFLGDGSGWGLFSDHPADFTPVCTTELGTLAKLDE 61

Qy 60 FTKKNCKLVGSCNDLQSHREWAKDIMAYAGRSNGLPPLVCDPNRELAASLGIMDPAEK 119
Db 62 FEKRVNKAIASVDDVESHKGIWKDINETQNTTVN--FPIIADKDKRVSELYGFIHFNAS 119

Qy 120 KKGGLPLTRCVRFFISPEKLAASILYPATTTGRNFAELRLVLDLSQLTAKFPVATPVDWT 179
Db 120 E-----TLTVRSILFVIDPKKKVRLIITYPASTGRNFDEVLRLVLDLSQLTDKHKVATPANWQ 175

Qy 180 AGAKCCVVPNLAAEF-AORLLPKGHEALQLPSGKPYLRLTPDP 221
Db 176 QGDDVIVPSLKDSEIIRKQPKGYTTV-----KPLYRLMTPOP 213

RESULT 39
ADN22014
ID ADN22014 standard; protein; 212 AA.
XX
XX AC ADN22014;
XX

DT 02-DEC-2004 (first entry)
 XX Bacterial polypeptide #4667.
 DE Recombinant DNA construct; transformed plant; improved plant property;
 XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX Bacteria.
 OS
 XX US2003233675-A1.
 PN
 XX 18-DEC-2003.
 PD
 XX 20-FEB-2003; 2003US-00369493.
 PF
 XX 21-FEB-2002; 2002US-0360039P.
 PR
 XX (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX WPI; 2004-061375/06.
 DR
 XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 PT
 XX Claim 1; SEQ ID NO 4667; 122pp; English.
 PS
 XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition. Improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 212 AA;
 Query Match 41.3%; Score 493.5; DB 8; Length 212;
 Best Local Similarity 45.9%; Pred. No. 8.8e-47;
 Matches 102; Conservative 37; Mismatches 70; Indels 13; Gaps 5;
 QY 1 MFLNLGDSFPDQAEALGAEHRLHEYLGDWSGWMFSDHNDFTFVCTTELAEAVKLQDSF 60
 DB 1 MSLRLGDIADPFRQK-SVGPFRFHWLGDWSGWLFSHPADFTFVCTTELGAKLAGEF 59

QY 61 TKKCKLVGFCSCNDLQSHREWAKDIMAYAGRSNLPFPLVCDPNRELAASLGIMDAEKD 120
 DB 60 EKRNVKTIALSVDSAESHKWKID1--NETQAANVGFPILADGDRKVSLEYDMIHFNANE 117
 QY 121 KKGLPLTCRCVFFISPEKLAASILYPATTGRNFAILRVLDLSQLTAKFPFVATPVDDTA 180
 DB 118 ----TLTVRSLSFVIDPKKVRLLIYPASTGRNFDVLRVIDLSQLTDSHVSATPQWKKQ 173
 QY 181 GAKCCVVPNLAABE-AQRLLPKGHEALQLPKGPYLRLPDP 221
 DB 174 GDVVIVPSLKDDEIIRKQKPKGYKAL-----RPVLRMTQP 210
 RESULT 40
 IDN24773
 ADN24773 standard; protein; 212 AA.
 XX
 AC ADN24773;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Bacterial polypeptide #7426.
 XX
 KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX
 OS Bacteria.
 XX
 PN US2003233675-A1.
 XX
 PD 18-DEC-2003.
 XX
 PF 20-FEB-2003; 2003US-00369493.
 XX
 PR 21-FEB-2002; 2002US-0360039P.
 XX
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX WPI; 2004-061375/06.
 DR
 XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 PT
 XX Claim 1; SEQ ID NO 7426; 122pp; English.
 PS
 XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition. Improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 212 AA;
 Query Match 41.3%; Score 493.5; DB 8; Length 212;
 Best Local Similarity 45.9%; Pred. No. 8.8e-47;
 Matches 102; Conservative 37; Mismatches 70; Indels 13; Gaps 5;
 QY 1 MFLNLGDSFPDQAEALGAEHRLHEYLGDWSGWMFSDHNDFTFVCTTELAEAVKLQDSF 60
 DB 1 MSLRLGDIADPFRQK-SVGPFRFHWLGDWSGWLFSHPADFTFVCTTELGAKLAGEF 59

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